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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: December 15, 2004, 18:05:00; Search time 122.151 Seconds

(without alignments)

804.673 Million cell updates/sec
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Title:
US-09-819-371-5
Perfect score: 274
Sequence: 1 GSHSLRYFSTAVSRPGRGEP......QRYTCHVQHEGLPQPLILRW 274
Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0 Searched: 2002273 segs, 358729299 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2002273

Post-processing: Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000 A Geneseq 236ep04:*

1: geneseqp1990s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003s:*
7: geneseqp203s:*
8: geneseqp203s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Human can HLA-Cw ov Fragment Human sec Human ova Human gen Human gen Human gen Lung canc Consensus Protein e HLA-C exo Marker ge Protein e Human hea Human can Human can Human apo Human HLA Human hla Aag64618 Human can hum Human can Breast ca Novel Description Aag64617 AAE55528 AAE55528 Adj72372 Adj72372 Adj72372 AAG56726 Aag64619 Aag64619 Aag64619 AAG55589 AAG55589 AAG5569 AAG65789 AAG65789 AAG65789 AAG66639 Aap80911 Adp12521 Adp65326 Adp65316 Aar12466 SUMMARIES AAG64618 ADF55588 ABB50296 ADP12500 AAG64619 ABO60639 AAG64617 ADJ70081 AAB43986 ABP42931 ADP12521 Query Match Length DB Score 4447034 444401 Result Š

0

0; Gaps

1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 60

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Query Match 100.0%; Score 274; DB 4; Length 274; Best Local Similarity 100.0%; Pred. No. 7.5e-250; Matches 274; Conservative 0; Mismatches 0; Indels C

Aaol3073 Human pol	_	Aab90793 Human she	Adi80341 Human leu	Ade31177 Human dia	Abo57118 Human gen	Adp29434 Human sec	Adf69311 Human lun	Adh48788 NOV31 pro	Ade40250 Human NOV	Aam18379 Peptide #		Aam30858 Peptide #		Abb22707 Protein #	Aam70538 Human bon	Aam58091 Human bra	Abg52217 Human liv	Aam05976 Peptide #	Abg40192 Human pep	,
AA013073	AAU32883	AAB90793	ADI80341	ADE31177	ABO57118	ADP29434	ADF69311	ADH48788	ADE40250	AAM18379	ABB37410	AAM30858	ABB32163	ABB22707	AAM70538	AAM58091	ABG52217	AAM05976	ABG40192	
374 4	380 4	120 4			-							-	91 4		H	91 4	Ġ		-	
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ALIGNMENTS

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This invention relates to a cancer cell specific HLA-F antigen. The invention includes DNA encoding the antigen, and a method for the preparation of the cancer cell specific HLA-F antigen. The antigen may be used in a method to diagnose cancer, in which the protein is used to detect anti-HLA-F antibodies in bodily fluids of the patient. The present sequence represents the cancer cell-specific HLA-F antigen of the invention.
                                                                                                                                                                                                                                                                                                                                                                                        Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
                                                                                                       Human cancer cell specific HLA-F antigen SEQ ID 5.
                                                                                                                                HLA-F antigen; cancer cell specific; human.
                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 10-11; 12pp; Japanese.
                         AAG64618 standard; protein; 274 AA.
                                                                                                                                                                                                                                         99JP-00279566.
                                                                                                                                                                                                                                                                   99JP-00279566.
                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                               WPI; 2001-360493/38.
N-PSDB; AAH45556.
                                                                                                                                                                                                                                                                                          (EGAW/) EGAWA K.
(MEDI-) MEDINET KK.
                                                                                                                                                                                                                                                                                                                      (KIMU/) KIMURA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 274 AA;
                                                                                                                                                                                    JP2001095584-A.
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                                                                                                                                                           Homo sapiens
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RESULT 1
AAG64618
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Gaps ö

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0; Mismatches

274; Conservative

Matches

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181. RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGBEQTQDTBLVETRPAGDGT

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AAG64617 standard; protein; 362

AAG6461 RESULT

121 KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ 180

121 KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ 181 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWORDGEEQTODTELVETRPAGDGT

1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW

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The present invention relates to an agent for preventing or treating cancer. The agent comprises a portion or a complete sequence of a human leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of presenting a cancer-cell specific antigen transformed with HLA-F DNA, or a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte (CTL) inducer which induces CTL which is non-specific to an organ, is unrestricted to the major histocompatibility complex (MHC) and specific to a cancer cell, and an anti-HLA-F antibody. The agent of the invention is useful for treating or preventing cancer. A cell capable of presenting a cancer-cell specific antigen is useful for measuring HLA-F antigen and for diagnosing cancer. The present sequence represents part of the human cancer-cell specific HLA-F antigen.
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                                                                                                          EWITGYAKANAQIDRVALRNILRRYNQSBAGSHILQGMNGCDMGPDGRLLRGYHQHAYDG 120
                       9
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                       GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                   EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
                                                                                                                                                       KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGGECLELLRRYLENGKETLQ
                                                                                                                                                                                         121 KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ
                                                                                                                                                                                                                                                                                  181 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWORDGEEOTODTELVETRPAGDGT
Agent for preventing and treating cancer, comprising human leukocyte antigen-F DNA, or a plasmid or viral vector comprising the DNA.
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                                                                                                                                                                                                                                                                                                                                                                     241 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADF55588 standard; protein; 274 AA
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N-PSDB; ADF55585.
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(MEDI-) MEDINET KK.
(KIMU/) KIMURA Y.
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100.0%; Pred. No. 9.4e-250;
ive 0; Mismatches 0;
                                                                   Human cancer cell specific HLA-F antigen SEQ ID
                                                                                             HLA-F antigen; cancer cell specific; human.
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                                      (first entry)
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(MEDI-) MEDINET KK.
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            AAG64617;
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Length 274;

Score 274; DB 7; Pred. No. 7.5e-250;

100.0%;

Query Match Best Local Similarity

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Ovarian tumour marker gene, human, overexpression; upregulation; epithelial tumour; cancer; diagnosis; prognosis; disease monitoring; identification; earous cystadenoma; borderline serous tumour; serous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenocarcinoma; mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma; undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma; denofibroma; Brenner tumour; serial analysis of gene expression; SACB; immune response pathway; cell proliferation regulation; protein folding; membrane localised; secreted; therapeutic target; cytostatic;
EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120
                           EWITGYAKANAQIDRVALRNLIRRYNQSEAGSHTLQGMNGCDMGPDGRLIRGYHQHAYDG 141
                                                                                   KDYISINEDLRSWTAADTVAQITQRFYEAEEFRTYLEGECLELLRRYLENGKETLQ 180
                                                                                                                                                                                                             RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting and identifying ovarian tumor, identifying increased risk for developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor marker
                                                                                                                          KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEBFRTYLEGECLELLRRYLENGKETLQ
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The methods can additionally be used to identify a particular tumour as being an ovarian tumour (i.e., an epithelial ovarian tumour selected from serous cystadenoma, borderline serous tumour, muchous cystadenoma, borderline serous tumour, muchous cystadenoma, borderline serous tumour, muchous cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma, clear cell adenocarcinoma, endometrioid carcinoma, adenofibroma and Brenner tumour. The ovarian tumour marker genes of the invention were identified using SAGE (serial analysis of gene expression) and were found to be using SAGE (serial analysis of gene expression) and were found to be using sAGE (serial analysis of gene expression) and were found to be relative to normal ovarian epithelial cells. The marker genes are implicated in immune response pathways, in the regulation of cell progliferation and in protein folding, and many of these are membrane corliferation and in protein folding, and many of these are membrane. Inclined or secreted. In addition to their use as diagnostic and prognostic markers, the ovarian tumour marker genes or their encoded prevention of ovarian cancer. Sequences ABBSOSS7-ABBSOS99 represent proteins encoded by ovarian tumour marker genes of the invention
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100.0%; Pred. No. 9.4e-250;
ative 0; Mismatches 0;
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(MEDI-) MEDINET KK.
(KIMU/) KIMURA Y.
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The present invention relates to an agent for preventing or treating cancer. The agent comprises a portion or a complete sequence of a human leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of presenting a cancer-cell specific antigen transformed with HLA-F DNA, or a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte (CTL) inducer which induces CTL which is non-specific to an organ, is unrestricted to the major histocompatibility complex (MHC) and specific to a cancer cell, and an anti-HLA-F antibody. The agent of the invention is useful for treating or preventing cancer. A cell capable of presenting a cancer-cell specific antigen is useful for measuring HLA-F antigen and for diagnosing cancer. The present sequence represents human cancer-cell specific antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 EWITGYAKANAQTDRVALRNILIRRYNQSEAGSHTLQGMNGCDMGPDGRILIRGYHQHAYDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 EWITGYAKANAQIDRVALRNILRRYNQSEAGSHILQGMNGCDMGPDGRLLRGYHQHAYDG 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDIQFLRFDSDAAIPRMEPREPWVRQEGEQYW 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bronchial asthma, chronic obstructive pulmonary disease, respiratory epithelial cell; interleukin-13; respiratory, antiasthmatic; gene therapy, marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RADPPKAHVAHHPISDHEATLRCWALGFYPABITLTWQRDGEEQTQDTSLVBTRFAGDGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                             Agent for preventing and treating cancer, comprising human leukocyte antigen-F DNA, or a plasmid or viral vector comprising the DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 274; DB 7; Length 362; 100.0%; Pred. No. 9.4e-250; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marker gene related amino acid sequence SEQ ID NO:624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 FOKWAAVVVPSGEEORYTCHVQHEGLPOPLILRW 274
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                                                                                                                        Claim 5; SEQ ID NO 4; 19pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ75372 standard; protein; 362 AA
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20-MAR-2003; 2003JP-00077212.
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WPI; 2003-486263/46.
N-PSDB; ADF55584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 362 AA;
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The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises or chronic obstructive pulmonary disease. The method comprises or chronic obstructive pulmonary disease. The marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. Also described: (1) a reagent (1) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (5) a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease; (6) a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, comprising the compound, a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene, a ribozyme, a polymucleotide that suppresses the expression of the gene through an RNAi effect or an antibody recognising a protein encoded by a marker gene; and (7) a DNA chip for testing for a proceding asthma or a chronic obstructive pulmonary disease, on which a proceding activities, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic agent invention.

Expense of the exemplification of the present invention.
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                                                                                                                                                   disease by
                                                                                                                                                   Testing for bronchial asthma or chronic obstructive pulmonary disease by comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a
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                                                    Kubo H, Nagai H, Izuhara K;
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100.0%; Pred. No. 9.4e-250;
:ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                               Example 11; SEQ ID NO 624; 241pp; English.
                                                    Ohtani N, Sugita Y, Yamaya M,
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(GENO-) GENOX RES INC.
                                                                                                   WPI; 2004-193155/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 362 AA;
                                                                                                                                                                                                                                healthy subject.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of
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                                                                                                                                                                                                            transplant rejection; immune system; rheumatoid arthritis; lupus; inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
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                                                                                                                                    Protein encoded by mRNA of the invention #110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 65; SEQ ID NO 2509; 1762pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EXPR-) EXPRESSION DIAGNOSTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-DEC-2002; 2002US-00325899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-APR-2003; 2003WO-US012946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-APR-2002; 2002US-00131831
                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosenberg S;
                                                                    12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the genes.
ADP12500;
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This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial concephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRP) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypepide sequence is a human heart mitochondrial protein of the invention.
                                                                                                                                                                                                                                                                  Huntington's disease; osteoarthritis;
Leber's hereditary optic neuropathy; LHON;
mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
osteopathic; ophthalmological; cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating with the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                Human heat mitochondrial protein as a therapeutic target SeqID1887.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glenn GM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 442;
                                                                                                                                                                                                                                                      mitochondrial; human; screening assay; diabetes mellitus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Taylor SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 274; DB 7; L
100.0%; Pred. No. 1.1e-249;
trive 0; Mismatches 0;
262 FOKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gibson BW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1887; 180pp; English.
                                                                                             ADJ70081 standard, protein; 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fahy ED, Zhang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-APR-2002; 2002US-0372843P.
17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-APR-2003; 2003WO-US010870.
                                                                                                                                                                       06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BUCK-) BUCK INST AGE RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              274; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-845369/78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 442 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003087768-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MITO-) MITOKOR
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-OCT-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Warnock DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ghosh SS,
                                                                                                                                   ADJ70081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                       RESULT 8
ADJ70081
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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
                           EWITGYAKANAQTDRVALRNILRRYNQSBAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 141
                                                                                  KDYISLNEDLRSWTAADTVAQITQRFYEAEBYAEBFRTYLEGECLELLRRYLENGKETLQ 180
EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120
                                                                                                                         142 KDYISLNEDIRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLEIIRRYLENGKETLQ 201
                                                                                                                                                                                                             202 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT 261
                                                                                                                                                                       RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                         FOKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274
                                                                                                                                                                                                                                                                                           262 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID NO 57085; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #26717
                                                                                                                                                                                                                                                                                                                                                                                                     ABG26726 standard; protein; 677 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-00540217, 23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS90913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200175067-A2.
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61
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                                                                                                                                                                                                                                                            331 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 390
                                                                                                                                                                                                                                                                                                61 EWITGYAKANAQTDRVALRNILRRYNQSEAGSHTLQGMNGCDMGPDGRLIRGYHQHAYDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                   451 KDYISLNEDLRSWTAADTVAQITQRFYEASEYAEEFRTYLEGECLELLRRYLENGKETLQ 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 RADPEKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAGDGT 240
                                                                                                                                                                                                                                                                                                                                    391 EWITGYAKANAOTDEVALRAYDVSEAGSHILGGWNGCDMGFDGRILRGYHGHAYDG 450
                                                                                                                                                                                                                      9
amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ttp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidabetic; antiasthmatic; antirhematic; antiathritic; antiviral; antidiabetic; antiasthmaticy; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; haematopoletic cell disorder; autoimmune disorder; haematopoletic cell disorder; organ rejection; haemostatic; thrombolytic, cardiovascular disorder; infection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                               121 KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ
                                                                                                                                                                                                                      1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                                                                                                                                0; Gaps
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                                                                                                                                       91.2%; Score 250; DB 4; Length 677; 100.0%; Pred. No. 6.6e-227; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cancer associated protein sequence SEQ ID NO:1431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB43986 standard; protein; 271 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-MAR-2000; 2000WO-US005882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAR-1999; 99US-0124270P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-FEB-2001 (first entry)
                                                                                                                                                          Local Similarity 100.0
hes 250; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 FOKWAAVVVP 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             571 FOKWAAVVVP 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-587533/55.
                                                                                                   Sequence 677 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAC78195.
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                                                                                                                                            Query Match
                                                                                                                                                                                  Matches
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(EGAW/) EGAWA K.
(MEDI-) MEDINET KK.
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                                                                                                                                                                                                                         invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                          Query Match
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                   AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB4338 to AAB44239. The proteins can have activities based on the tissues and calls the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiaethmatic; antirheumatic; antidiator; antivities antibactor; antibactor; antibactor; antibactor; cagulant; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipactiatic and antiangingenic. The polymucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polymucleotides, polypeptides, antibodies, agonists and antagoniets from the proliferation, differantiation or mobilisation of inhibiting the proliferation, differantiation or mobilisation of inflammation, cancers cardiovascular disorders, neurological disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers cardiovascular disorders, neurological disease and papenserial or viral limeterinas. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78457 and AAB44240 represent sequences used in the exemplification of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDYISLNEDLRSWTAADTVAQITQRFYEASEYAEEFRTYLEGECLELLRRYLENGKETLQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267
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                                                                                                                                                                                                                                                                                                                                                                                                              28 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPREPRVEQEGPQYW 87
                                                                                                                                                                                                                                                                                                                                                                                                                                               EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 RADPPKAHVAHHPISDHEATLRCWALGFYPABITLTWQRDGEBQTQDTBLVETRPAGDGT
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                       88.0%; Score 241; DB 3; Length 271; 100.0%; Pred. No. 9.8e-219; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cancer cell specific HLA-F antigen SEQ ID 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLA-F antigen; cancer cell specific; human
Claim 11; Page 2115-2116; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG64619 standard; protein; 215 AA.
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                                                                                                                                                                                                                                                                                                                                                                  Matches 241; Conservative
                                                                                                                                                                                                                                                                                        the present invention
                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                Sequence 271 AA;
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AAG64619
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202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142
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                                                                                                                                            Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 IAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYWEWTTGYAKANAQTDRVALRNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IAVEYVDDIQFLRFDSDAAIPRMEPREPWVEQEGPQYWEWTIGYAKANAQIDRVALRNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 RRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDGKDYISLNEDLRSWTAADTVAQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 RRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDGKDYISLNEDLRSWTAADTVAQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 TORFYBAEEYAEBFRIYLEGECLELLRRYLENGKETLORADPPKAHVAHHPISDHEATLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fragment #2 of human cancer-cell specific HLA-F antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.5%; Score 215; DB 4; Le
100.0%; Pred. No. 2.7e-194;
ive 0; Mismatches 0;
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                                                                                                                                                                                                      Claim 1; Page 11-12; 12pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADF55589 standard; protein; 215 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-2002; 2002JP-00088991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-2001; 2001JP-00090121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-FEB-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 215; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-486263/46.
N-PSDB; ADF55586.
                                                         WPI; 2001-360493/38.
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(MEDI-) MEDINET KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MEDI-) MEDINET KA
(KIMU/) KIMURA Y.
(KIMU/) KIMURA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 215 AA;
                                                                                      N-PSDB; AAH45557
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The present invention relates to an agent for preventing or treating cancer. The agent comprises a portion or a complete sequence of a human leukocyte antigen (HiA-F DNA. Also disclosed is a cell capable of presenting a cancer-cell specific antigen transformed with HiA-F DNA, or a plasmid or viral vector comprising HiA-F DNA, a cytotoxic T lymphocyte (CTL) inducer which induces CTL which is non-specific to an organ, is unrestricted to the major histocompatibility complex (MHC) and specific to a cancer cell, and an anti-HiA-F antibody. The agent of the invention is useful for treating or preventing cancer. A cell capable of presenting a cancer-cell specific antigen is useful for measuring HiA-F antigen and for diagnosing cancer. The present sequence represents part of the human cancer-cell specific HiA-F antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RRYNOSBAGSHTLOGMNGCDMGPDGRLLRGYHQHAYDGKDYISLNBDLRSWTAADTVAQI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TORFYEAEEYABEPRTYLEGECLELLRRYLENGKETLORADPPKAHVAHHPISDHEATLR 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 IAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYWEWTTGYAKANAQTDRVALRNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IAVEYVDDIQFLRFDSDAAIPRMEPREPWVEQEGPQYWEWTTGYAKANAQTDRVALRNLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDGKDYISLNEDLRSWTAADTVAQI
Agent for preventing and treating cancer, comprising human leukocyte antigen-F DNA, or a plasmid or viral vector comprising the DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
                                                                                                                                                                                                                                                                                                                                                                                n 78.5%; Score 215; DB 7; Length 215; Similarity 100.0%; Pred, No. 2.7e-194; 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 CWALGFYPAEITLIWQRDGEEQTQDTELVETRPAG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 CWALGFYPAEITLIWORDGEBOTODTELVETRPAG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein, SEQ ID NO: 4290.
                                                       Claim 7; SEQ ID NO 6; 19pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG00209 standard; protein; 120 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-FEB-2000; 2000EP-00200610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 215; Conservative
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                                                                                                                                                                                                                                                                                                                                                 Sequence 215 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAC00215
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                                                                                                                                                                                                                                                                                                                                                                                                       Local
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The present sequence is a polypeptide encoded by one of a large number of program defined from RNMs encoding secreted proteins. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (URR) of the mRNA because they are often obtained from oligo-draprimed cDNA libraries. Such ESTS are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where included. S' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, game therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; infilammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antinflammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GSHSLRYFSTAVSRPGRGEPRYIAVBYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                     Claim 13; SEQ ID NO 4290; 71pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 EWITGYAKANAQIDEVALRNILERRYNQSEAGSHILQGMN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 EWITGYAKANAQIDRVALRNLLRRYNQSEAGSHTLQGMN 99
                                                                                                                                                                                                                                                                                                                                                                                                              36.1%; Score 99; DB 3; Le
100.0%; Pred. No. 4.3e-85;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ovarian antigen HPDRT37, SEQ ID NO:4063.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABP42931 standard; protein; 186 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-JUN-2000; 2000US-0209467P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-2001; 2001WO-US018569.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-147878/19.
N-PSDB; ABQ56008.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birse CE, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                        Sequence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200200677-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP4328) and to cDNAs encoding them (ABP4131-ABP56305), and also encompasses polypeptides 90% identical and polymotechides 93% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens to polymotechides, antibodies against human ovarian antigens and the use of ovarian antigen polymotechides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Buch conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system of sorders (e.g., infertility, disorders of pregnancy, anovulation.) polycystic ovary syndrome, ovarian orpsets, and dysmenorines of polycystic ovary syndrome, ovarian orpsets, and dysmenorines, infertions (e.g., chiamydia, HIV, toxoplasmosis, and toxic shock syndrome, organities, systemic lupus erythematosus), blood-related disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oobhorities, systemic lupus erythematosus), blood-related disorders. (e.g., anaemia), cardiovascular disorders, nucrological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polypeptides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polymucleotides may be used for gene therapy, chromosome mapping, in the present squence represents a human ovarian antigen of the prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the propertices are the propertices.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 YAKANAQTDRVALRNILLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDGKDYIS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YAKANAQIDRVALRNILRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDGKDYIS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
cancer), immune disorders, cardiovascular disorders and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 25.5%; Score 70; DB 5; Length 186; Best Local Similarity 100.0%; Pred. No. 1.3e-57; Matches 70; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, gene expression, single exon probe, microarray, alternative splicing event, genomic alteration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome derived single exon protein #3318.
                                                              Claim 11; SEQ ID NO 4063; 2922pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABOS7084 standard; protein; 96 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2003194704-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 186 AA;
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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6808 amino acid sequences ("Illy defined in the specification. The probe is a single exon probe that bybridises under high stringency conditions to a nucleic acid molecule expression (comprising a plurality of single exon mucleic acid molecule expression (comprising a plurality of single exon nucleic acid adressably isolatable or amplifiable from the plurality), a single and addressably isolatable or amplifiable from the plurality), a single contiguous amino acids of any of the above. mentioned amino acid exon probes contiguous amino acids of any of the above. mentioned amino acid sopposition and addression acids of any of the above. mentioned amino acid soppositionally with conservative amino acid substitutions), and sequences (optionally with conservative amino acid substitutions), and econtiguous amino acids of any of the above. mentioned amino acid substitutions), and accomplisated antibody that binds specifically to a peptide cited above.

Contiguous amino acids of any of the above mentioned amino acid substitutions), and accomplisated antibody that binds specifically to a peptide cited above. The probes may be used as tools for surveying a customer desiring to measure gene expression, and accompleter-readable cited above. The probes may be used as tools for surveying to expression analysis. The probes may be used as tools for surveying to expression analysis. The probes may be used as tools for surveying to expect the probes may be used as tools for surveying alternative splicing events, in detecting and characterising according and contains a detabase having a plurality of according to expression and acterious, in priming the synchologome, the probes are used in identifying and characterising and alternative splicing events, in detecting and characterisin
                                                                                                                                                                               New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 DPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGTFQ 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 DPPKAHVAHHPISDHEATLACWALGFYPABITLIWQRDGEEQTQDTELVETRPAGDGTFQ 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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6.1e-56;
hes 0; Indels
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                                                                                                                                                                                                                                                                                                 Claim 45; SEQ ID NO 30718; 80pp; English.
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                                                                                           Penn SG, Rank DR, Hanzel DK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 KWAAVVVP 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 KWAAVVVP 69
                                                                                                                                     WPI; 2004-119264/12.
(PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 68; Conserv
                                                                                                                                                                                                                                                          surveying tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 96 AA;
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Sequence 5, Appli
Sequence 183, Appl
Sequence 1431, Ap
Sequence 4, Appli
Sequence 6, Appli
Sequence 3018, A
Sequence 3018, A
Sequence 31089, A
Sequence 315, Appli
Sequence 315, Appli
Sequence 815, Appli
Sequence 815, Appli
                                                                                                                       December 15, 2004, 18:24:34 ; Search time 111.505 Seconds (without alignments) 877.689 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                   274
1 GSHSLRYFSTAVSRPGRGEP......QRYTCHVQHEGLPQPLILRW 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

17: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

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10: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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4 US-10-257-021-82

US-10-408-758-76

US-09-925-301-1431

1 US-09-819-371-4

1 US-09-819-371-4

1 US-08-819-371-4

5 US-10-264-049-4063

4 US-10-29-386-30718

US-10-029-386-31089

US-10-925-302-835

US-09-925-302-835

US-09-925-302-835

US-10-430-984-16
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                                                                                  OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                          Sequence:
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RESULT 1 US-09-819-371- Sequence 5, Publication GENERAL INFO TITLE OF IN	9-371-5 ce 5, App L INFORM L INFORM L INFORM CANT; EG CP INVE OF INVE NT FILIN NT STA	SULT 1 1.09-819-371-5 Sequence 5, Application US/098 Sequence 5, Application US/098 Publication No. US20040053344A GENERAL INFORMATION: APPLICANT: BGAWA, KOhji TITLE OF INVENTION: Using Th FILLE REPERENCE: 30815 FILLE REPERENCE: 30815 CURRENT APPLICATION UMBER: U CURRENT APPLICATION UMBER: U CURRENT FILING DATE: 2020-03 NUMBER OF SEQ ID NOS: 6 SEQ ID NO 5 LENGTH: 274 TYPE: PRT ORGANISM: HOMO SapienS	m US/(0533-34); OS333-44); Maing Tumber 2002-2002-118ion	0981 44A1 Cell Thee	ALIGNMENTS 9371 -Specific HLA-F Antigen reof (09/819,371 15	and a Diagnostic Method of Can
Query Match Best Local S Matches 274 Qy 1 Db 1 Qy 61	1 GS 1 GS 1 GS 1 GS 1 GS 1 GS 1 GS 1 EW 61 EW	Similarity 4; GHICRESTA GHILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	100 1000 ative AVSRPC AVSRPC AQTORY	.0%; .0%; .0%; .0%; .0%; .0%; .0%; .0%;	100.0%; Score 274; DB 11; Length 274; Conservative 100.0%; Pred. No. 2.6e-260; Conservative 0; Mismatches 0; Indels 0; Gaps GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWYEQEGPOYM GIHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	th 274; 18 0, Gaps 0; 19 11

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181 RADPPKAHVAHHPISDHBATLRCWALGFYPAEITLTWQRDGBEQTQDTELVETRPAGDGT 240
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| Publication No. US20040101874A1
| GENERAL INFORMATION: US20040101874A1
| APPLICANT: GROSH, Soumitra S. | APPLICANT: Eaby, Eain D. | APPLICANT: Eaby, Eain D. | APPLICANT: Taylor, Bradford W. | APPLICANT: Taylor, Steven W. | APPLICANT: Taylor, Steven W. | APPLICANT: Warnock, Dale E. | TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIAL PROTECME | TITLE OF INVENTION: DENTIFIED IN THE MITOCHONDRIA
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                                                                                                                                                                                                                                                                                                                                   Sequence 82. Application US/10257021
Publication No. US20030211498A1
GENERAL INFORMATION:
APPLICANT: Morin. Patrice J.
APPLICANT: Sherman-Baust, Cheryl A.
APPLICANT: Hough, Colleen D.
ITLLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER;
FILE REFERENCE: 14014.0369U2
CURRENT APPLICATION NUMBER: US/10/257,021
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: PCT/US01/10947
PRIOR APPLICATION NUMBER: 60/194,336
PRIOR APPLICATION NUMBER: 60/194,336
PRIOR APPLICATION NUMBER: 60/194,336
NUMBER OF SEQ ID NOS: 147
SEQ ID NO 822
INNOW APPLICATION NUMBER: 60/194,336
NUMBER OF SEQ ID NOS: 147
SEQ ID NO 822
                                                                               241 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
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Matches 274; Conservative
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; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-257-021-82
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US-10-408-765A-1887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 KDYISLNEDLRSWTAADTVAQITQRFYEAEBYAEBFRTYLBGECLELLRRYLENGKETLQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 RADPPKAHVAHHPISDHEATLRCWALGFYPABITLITWQRDGEEQTQDTELVETRPAGDGT 240
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                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 274; DB 16; Length 442;
Best Local Similarity 100.0%; Pred. No. 3.9e-260;
Matches 274; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies;
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies;
FILE REPERENCE: PA106
CURRENT APPLICATION NUMBER: US/05/925,301
CURRENT PILING DATE: 2001-08-10
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOUTHWARE: Patentin Ver. 2.0
SEQ ID NO 1431
LENGTH: 271
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Best Local Similarity 100.0%; Pred. No. 6.3e-228;
Matches 241; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 FOKWAAVVVPSGEEORYTCHVQHEGLPOPLILRW 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 FOKWAAVVVPSGEBORYTCHVQHEGLPOPLILRW 295
CURRENT APPLICATION NUMBER: US/10/408,765A CURRENT FILING DATE: 2003-04-04 NUMBER OF SEQ ID NOS: 3077 SOFTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO 1887 LENGTH: 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 1431, Application US/09925301; Patent No. US20020052308A1; GENERAL INFORMATION:
                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                    US-10-408-765A-1887
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US-09-925-301-1431
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LOCATION: (176\overline{\Gamma} -FIGURE INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids FERTURE:
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OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (107) OTHER INFORMATION: Kaa equals any of the twenty naturally occurring L-amino acids
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R INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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157 LQRADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAG 215
                                                                                                                                                                                                                                                      APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA133P1
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR PILING DATE: 2001-06-07
PRIOR FILING DATE: 2000-06-07
NUMBER OF SGQ ID NOS: 4360
SOPTWARE: Patentin Ver. 3.1
SEQ ID NO 4063
                                                                                                                                                                         ; Sequence 4063, Application US/10264049; Publication No. US20040005579A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (77) OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: MISC_FEATURE
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                                                                                                                  RESULT 7
US-10-264-049-4063
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Publication No. US20040053344A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can
TITLE OF INVENTION: Using Thereof
FILE REPERBYCE: 30815
CURRENT FILING DATE: 2002-03-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.0
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JERRAN KOHJI
TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can
TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can
TITLE REPERENCE: 30815
CURRENT APPLICATION NUMBER: US/09/819,371
CURRENT APPLICATION NUMBER: 2002-03-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.0
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                                    208 RADPPKAHVAHHPISDHEATLRCWALGFYPASITLIWQRDGSEQTQDTELVETRPAGDGT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 EWITGYAKANAQIDRVALRNILIRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 141
      RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GSHSLRYFSTAVSRPGRGEPRYIAVBYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
63.9%; Score 175; DB 11; Length 362;
Best Local Similarity 100.0%; Pred. No. 5.1e-163;
Matches 175; Conservative 0; Mismatches 0; Indels 0
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43.4%; Score 119; DB 11; Length 215;
Best Local Similarity 100.0%; Pred. No. 3e-108;
Matches 119; Conservative 0; Mismatches 0; Indels 0
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Publication No. US20040053344A1
GENERAL INFORMATION:
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                                                                                                                     241 F 241
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US-09-819-371-6
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Sequence 31089, Application US/10029386

Sequence 31089, Application US/10029386

Publication No. US200301947041

GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: UNMERS: US/10/029,386
CURRENT PELICATION NUMBER: US/10/029,386
CURRENT PILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOOFWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 31089
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| Sequence 835, Application US/09925302
| Sequence 835, Application US/09925302
| Patent No. US2000494941A1
| Patent No. US2000494941A1
| APPLICANT: Rosen et al.
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA104
| CURRENT APPLICATION NUMBER: US/09/925,302
| CURRENT PILING DATE: 2001-08-10
| PRIOR PILING DATE: 1999-03-12
| PRIOR FILING DATE: 1999-03-12
| NUMBER: OF SEQ 1D NOS: 896
| SOFTWARE: PatentIn Ver. 2.0
| SEQ 1D NO 835
                                                                                                                                                                                                                                                                                                                    Query Match 16.1%; Score 44; DB 14; Length 77; Best Local Similarity 100.0%; Pred. No. 5.1e-35; Matches 44; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 OTODIELVETRPAGDGTFOKWAAVVVPSGEEORYTCHVOHEGLP 267
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                                                                                                                          CTHER INFORMATION: MAP TO CHR6.1
CTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 53
CTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.4
CTHER INFORMATION: SMISSPROT HIT: P30507, EVALUE 6.00e-42
US-10-029-386-34273
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GOTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1

SOTHER INFORMATION: SMISSPROT HIT: P30509, EVALUE 1.00e-52
US-10-029-386-3108
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Matches 44; Conservative
                                     TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                     FEATURE:
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US-10-029-386-30718

Sequence 30718, Application US/10029386

Publication No. US20030194704A1

SETEMBLE INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENONE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR (TITLE OF INVENTION: HUMAN GENONE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR (TITLE OF INVENTION: HUMAN GENONE-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR (TITLE OF INVENTION: HUMAN GENONE-SION ANALYSIS TWO

TITLE OF INVENTION: ADDITION NUMBER: US/10/029,386

CURRENT APPLICATION NUMBER: 2001-12-20

CURRENT PILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
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Publication No. US2030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEPUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEPUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
GURRENT PILING DARE: 2001.12-20
CURRENT PILING DARE: 2001.12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annowmax Sequence Listing Engine vers. 1.1
; NAME/KEY: MISC_FEATURE
; LOCATION: (180)
US-10-244-049-4063
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                                                                                                                                                                                                                                                                                  66 YAKANAQIDRVALRNILLRRYNQSEAGSHTLQGNNGCDMGPDGRLLRGYHQHAYDGKDYIS 125
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                                                                                                                                                                                                                                                                                                                               1 YAKANAQIDRVALRNLIRRYNQSEAGSHTLQGMNGCDMGPDGRLIRGYHQHAYDGKDYIS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 DPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGTFQ 61
                                                                                                                                                                                                                                0; Gaps
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                                                                                                                                                        Ouery Match 25.5%; Score 70; DB 15; Length 186; Best Local Similarity 100.0%; Pred. No. 3.4e-60; Matches 70; Conservative 0; Mismatches 0; Indels
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24.8%; Score 68; DB 14; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.7e-58;
Matches 68; Conservative 0; Mismatches 0; Indels
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COTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6
COTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12
COTHER INFORMATION: SWISSPROT HIT: P30511, EVALUE 2.00e-52
US-10-029-386-30718
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ORGANISM: Homo sapiens
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US-10-029-386-34273
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LENGTH: 96
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Query Match
15.7%; Score 43; DB 17; L
Best Local Similarity 100.0%; Pred. No. 2.6e-33;
Matches 43; Conservative 0; Mismatches 0;
Query Match
15.7%; Score 43; DB 17; L
Best Local Similarity 100.0%; Pred. No. 2.5e-33;
Matches 43; Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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US-10-029-386-30752
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LENGTH: 78
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LENGTH: 500
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APPLICANT: The Beard of Trustees of the University of Arkansas
APPLICANT: Crew, Mark D
TITLE OF INVENTION: Genes Encoding Single Chain Human Leukocyte Antigen E (HLA-E)
TITLE OF INVENTION: Proteins to Prevent Natural Killer Cell-Mediated Cytotoxicity
FILE REFERENCE: 8793-53098
CURRENT APPLICATION NUMBER: US/10/430,984
CURRENT PILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.2
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                                                                                                     NAME/KEY: SITE 1 COATION: (95) CATAION: (95) COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-302-835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (95)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-302-835
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Publication No. US20030064072A9
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAIOA.
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
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                                                                                                                                                                                                                                          'Match 16.1%; Score 44; DB 9; Length 104; Local Similarity 100.0%; Pred. No. 6.7e-35; les 44; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                   224 QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 267
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                                                                                                                                                                                                                                                                                                                                                                                                 32 QIQDIELVETRPAGDGIFQKWAAVVVPSGEBQRYICHVQHEGLP 75
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16.1%; Score 44; DB 10; L
Best Local Similarity 100.0%; Pred. No. 6.7e-35;
Matches 44; Conservative 0; Mismatches 0;
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Publication No. US20040225112A1
GENERAL INFORMATION:
                                                    ORGANISM: Homo sapiens
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US-09-925-302-835
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US-10-430-984-16
  LENGTH: 104
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Sequence 30752, Application US/10029386

Sublication No. US20030194704A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G.
FILLE REPERENCE: ADOMICA.X.-2
CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                       US-10-430-984-15
Sequence 15. Application US/10430984
Sequence 15. Application WS/2004025512A1
GENERAL INFORMATION:
APPLICANT: THE BOARD of Trustees of the University of Arkaneas
APPLICANT: The Board of Trustees of the University of Arkaneas
TITLE OF INVENTION: Genes Encoding Single Chain Human Leukocyte Antigen E (HLA-E)
TITLE OF INVENTION: Proteins to Prevent Natural Killer Cell-Mediated Cytotoxicity
FILE REPERENCE: 8793-53098
CURRENT PILING DATE: 2003-05-09
CURRENT FILING DATE: 2003-05-09
NUMBER OF SEQ ID NOS: 16
SOOTHWARE: Patentin version 3.2
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Length 476;
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OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 8.7

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 48

OTHER INFORMATION: EXPRESSED IN FILL LIVER, SIGNAL = 11

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 57

OTHER INFORMATION: SWISSPROT HIT: P30507, EVALUE 7.00e-24
                                                          Indels
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                                                                                                                                                              364 TQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 406
                                                                                                                        225 IQDIELVETRPAGDGIFQKWAAVVVPSGEEQRYTCHVQHEGLP 267
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Search completed: December 15, 2004, 18:41:48 Job time : 112.505 secs

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Q70pl7 macaca mula
Q70pm0 macaca mula
Cad89636 macaca mu
Cad89639 macaca mu
Q9mxs6 macaca mula
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pan troglod
homo sapien
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homo sapien
homo sapien
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Q861f0 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                O6du28 homo sapien
Aah62991 homo sapi
                                                                                                                                                                                                                                                                                                                                                                                                                 homo sapien
pan troglod
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Bad18842 aotus tri
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                                                                                                                                                                                                                                                                                                                                                                                                                                Bac54915 homo sapi
                                              December 15, 2004, 18:05:30 ; Search time 111.677 Seconds (without alignments) 1107.709 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bac86108 homo sapi
                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             macaca
                                                                                                1 IAVEYVDDTQFLRFDSDAAI.....QRDGBEQTQDTELVETRPAG 215
                                                                                                                                                                                                                                                                                                                               Description
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095it2
08wlp5
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06du28
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Q29958
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                          1825181 segs, 575374646 residues
                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                               <u>0</u>6DU28
AAH62991
HLAF_HUMAN
QTYR27
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HLAF MACMU
Q30713
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1C28 PANTR
078094
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                              OM protein - protein search, using sw model
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Q95HC0
Q860R0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAD89636
                                                                                                                         Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                              Q861E9
Q861F0
Q8MGQ1
Q951T2
                                                                                                                                                                                                                                                                                                                                                                              Q8WLPS
Q6DU20
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                                                                                                                                                                                                                                   UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*
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Match Length DB
                                                                                 US-09-819-371-6
                                                                                                                                                                                                                                                                                                                                                               OLIGO
                                                                                         Perfect score:
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                                         Cad65766 macaca mu
Cad65767 macaca mu
Cad63767 macaca mu
Cad63073 macaca mu
Q6i7a3 macaca fasc
Q9mx5 macaca neme
Q860e9 macaca neme
Q860e7 macaca neme
Q70pk6 macaca mula
Cad69650 macaca mula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 DGKDYISLNEDIRSWTAADTVAQITQRFYBAEEFYAEEFRTYLEGGECLEILRRYLENGKET 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q70ue5 macaca mula
Q70ue6 macaca mula
Q70ue7 macaca mula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 LORADPPKAHVAHHPISDHEATLRCWALGFYPABITLTWQRDGBEOTGDTBLVETRPAG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 IQRADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAG 254
270sio macaca mula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                      Liu Y., Xu L., Zeng Y., He X.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY221102; AA034407.1;
CO; GO:0016620; C:membrane; IEA.
GO; GO:0016620; C:membrane; IEA.
InterPro; IPR00710; Ig-like.
InterPro; IPR007359; Ig_c1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003599; MHC_I.
Pfam; PF0129; MHC_I:
Pfam; PF0129; MHC_I:
Pfam; PF0129; MHC_I:
Pfam; PF00129; MHC_I:
Probom; PF00050; MHC_I:
Probom; PF00050; MHC_I:
PROSITE; PS00295; IG_LIKE; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 55.3%; Score 119; DB 2; Length 324; Best Local Similarity 100.0%; Pred. No. 5.9e-117; Matches 119; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             324 AA; 36518 MW; E3E028177D2716F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                       OL-UUN-2003 (TrEMBLrel. 24, Created)
Ol-UUN-2003 (TrEMBLrel. 24, Last sequence update)
Ol-MAR-2004 (TrEMBLrel. 26, Last annotation update)
MHC class I antigen (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 324 AA
                                                                                                                                                                                  ALIGNMENTS
         Q70UES
Q70UE6
Q70UE7
CAD65766
CAD65765
CAD65767
CAD83073
Q617A3
                                                                                                            Q860E9
Q860E7
Q70PK6
CAD89650
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SEQUENCE FROM N.A.
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Q861F0,
01-JUN-2003 (
01-JUN-2003 (
01-MAR-2004 (
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NON TER
SEQUENCE
 RESULT 2
Q861F0
ID Q8611
AC Q8611
DT 01-JI
DT 01-JI
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SEQUENCE FROM N.A.
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                                                                                                                                                                                     Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane
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                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 DGKDYISLNEDLRSWTAADTVAQIIQRFYEAEEYAEFRTYLEGECLELLRRYLENGKET 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 LORADPPXAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAG 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E., Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                             # EX., Xu L., Liu Y., Zeng Y.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY216682; AAO37689.1; --
HSSP; Q29961; HR9.
R GO; GO:0016020; C:membrane; IEA.
R GO; GO:0016020; C:membrane; IEA.
R GO; GO:0016020; C:membrane; IEA.
R InterPro; IPR003597; Ig c1.
R InterPro; IPR003506; Ig MHC.
R InterPro; IPR003069; Ig C1.
R Pfam; PF07654; C1-set; 1.
R PRINTS; PR01638; MHC I; 1.
R PRINTS; PR01638; MHC I; 1.
R PRINTS; PR01638; MHC I; 1.
R PRNOSTE; PS00050; IG MHC; 1.
R PROSTE; PS00035; IG LIKE; 1.
R PROSTE; PS000290; IG MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.3%; Score 119; DB 2; Length 324; 100.0%; Pred. No. 5.9e-117; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 23 | SECURICE FROM N.A. | Moore Y.F., Geraghty D.E.; A SUDURICE FROM N.A. | Moore Y.F., Geraghty D.E.; BYO C.-W., Ishitani A., Moore Y.F., Geraghty D.E.; BYO C.-W., Ishitani A. | Moore Y.F., Geraghty D.E.; BYO C.-W., Ishitani A. | Moore Y.F., Geraghty D.E.; BYO C.-W., Ishitani A. | Moore Y.F. | Moore 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       324 324
324 AA; 36518 MW; E3E028177D2716F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QBMGQ1 PRELIMINARY, PRT, 346 AA. QBMGQ1; CTC22002 (TrEMBLrel. 22, Created) 01-0CT-2002 (TrEMBLrel. 22, Last sequence update) 01-0CT-2004 (TrEMBLrel. 28, Last annotation update) MHC class Ib antigen.
Nonclassical MHC class I antigen (Fragment). Name=HLA-F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119; Conservative
                                                Homo sapiens (Human)
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                                                                                                                                                  SEQUENCE FROM N.A.
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 DGKDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKET 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 DGKDYISLNEDLRSWTAADTVAQITQRFYEABESTABEFRTYLEGECLELLRRYLENGKET 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 55.3%; Score 119; DB 2; Length 346; Best Local Similarity 100.0%; Pred. No. 6.3e-117; Matches 119; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          346 AA; 39061 MW; D4782968A67E9B7D CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 346 AA.
InterPro; IPR0013006; Ig_MHC.
InterPro; IPR001039; MHC_I.
Pfam; PF00129; MHC_I: 1.
PRINTS; PR01638; MHCCLASSI.
ProDom; PR001050; MHC_I: 1.
PROSTUR; SM0407; IGG1; I.
PROSTUR; PS50835; IG LIKE; I.
PROSTUR; PS00290; IG_MHC; I.
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MEDLINE=238825; PubMed=12477932;

Strausberg R.L. Feingold E.A., Grouse L.H., Derge J.G.,

A Klausner R.D., Colline F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Klausner R.D., Colline F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Rabachul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heishe F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Sapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheez T.E.,

Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

A Nilalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,

A Nilalon D.K., Mazny D.W., Sodergren B.J., Lu X., Gibbs R.A.,

A Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G.,

A Hiting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
200 LORADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAG 258
                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo,
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.,
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  He X., Xu L., Liu Y., Zeng Y.; "Identification of a novel HLA-F allele - HLA-F*010102."; Tissue Antigens 63:181-183(2004).
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AF523285; AAW74980.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                He X., Xu L., Liu Y., Zeng Y.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
MMC class 1b antigen (HLA-F protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                         PRT;
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EMBL, AF523293, AAM74988.1;
EMBL, AF523294, AAM74989.1;
EMBL, AF523295, AAM74990.1;
EMBL, AF523295, AAM74991.1;
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                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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FISSUE=Lymph;
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                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=14705989;
                                                                                                                                                                                                                                                                          Name=HLA-F;
                                                                                                                      OBWLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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Pro C.-W., Ishitani A., Moore Y.F., Geraghty D.E.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY645755; AAT173238.1;
SEQUENCE 346 AA; 39082 MW; 6F739AA41917E7B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346 AA; 39051 MW; D4782AA4697D57B2 CRC64;
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Pred. No. 6.3e-117;
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v 100.0%; Pred. No. e...
o; Mismatches
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GO; GO:0016021, C:integral to membrane; IEA.

GO; GO:0006955; P:immune response; IEA.

InterPro; IPR007110; IG-1ike.

InterPro; IPR003006; IG-MC.

InterPro; IPR001039; MHC.
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                                                                                                                                                                                             AAT73239.1; -.
                                                                                                                                                                                                           AAT73240.1; -.
                                                                                                                                                                                                                                                                AAM74981.1; -.
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AAH62991.1;
                                                                                                                                                         AAT73235.1;
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Pfam; PF00129; MHC I; 1.
PRINTS; PR01638; MHCLASSI.
ProDom; PD000050; MHC I; 1.
SWART; SW00407; IGC1; 1.
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                                                                                                                                                                                                                                                                               Q29961; 1HSA
                                                                                                EMEL, AY645749,
EMEL, AY645750,
EMEL, AY645751,
EMEL, AY645751,
EMEL, AY645753,
EMEL, AY645756,
EMEL, AY645756,
EMEL, AY645756,
EMEL, AY645759,
EMEL, AY645759,
EMEL, AY645759,
EMEL, AY645759,
EMEL, AY645759,
EMEL, AY645759,
                                                   AY645744;
 BC062991;
                  AY645742;
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Q6DU20;
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EMBL;
EMBL;
EMBL;
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MEDLINE=22388257; PubMed=12477932;
MEDLINE=2238257; PubMed=124782;
MEDLINE=238257; PubMed=124782;
MEDLINE=238
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140 DGKDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKET 199
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                                                                                     157 LORADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAG 215
                                                                                                                                             200 LORADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEBOTODTELVETRPAG 258
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.3%; Score 119; DB 2; Length 346; 100.0%; Pred. No. 6.3e-117; ive 0; Mismatches 0; Indels
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Submitted (UUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY645747; AAT732230.1;
SEQUENCE 346 AA, 39079 WW, 82370BFB40B15818 CRC64;
                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=HLA-F;
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AAH62991;
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Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20189617; PubMed=10727083; Hampe A., Coriton O., Andrieux N., Carn G., Lepourcelet M., Calibert F., Moctier S., Dreano S., Gatius M.T., Hitte C., Soriano N., Galibert F., "A 356-Kb sequence of the subtelomeric part of the MHC class I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ξ
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01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last Sequence update)
05-UDL-2004 (Rel. 44, Last annotation update)
HIA Class I histocompatibility antigen, alpha chain F precursor (HLA antigen) (Leukocyte antigen F) (CDA12).
Name=HLA-F; Synonyms=HLAF, HLA-5.4;
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MEDIINE=90111605; Pubmed=1688605;

MEDIINE=90111605; Pubmed=1688605;

MEDIINE=90111605; Pubmed=1688605;

MEDIINE=90111605;

MEDIINES DEL, Well X., Orr H.T., Koller B.H.;

"Human leukcoyte antigen F (HIA-F). An expressed HLA gene composed a class I coding sequence linked to a novel transcribed repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND VARIANT PRO-272.
MEDLINE-22935763; PubMed=14574404; DOI=10.1038/nature02055;
Mungall A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L.,
Wilming L., Jones M.C., Horton R., Hunt S.E., Scott C.E.,
Gilbert J.G.R., Clamp M.E., Bethel G., Milne S., Ainscough R.,
Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S.,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Lury D., Epstelah H., Holmes N.;
"The human class I MHC gene HLA-F is expressed in lymphocytes.";
Int. Immunol. 2:531-537(1990).
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                                                                                                                                                                                                                                                Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC062991; AAH6291.1; -
SEQUENCE 346 AA; 39051 MW; D4782AA4697D57B2 CRC64;
                                                                     ind mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                          SEQUENCE FROM N.A. TISSUE=Lymph;
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                                                                     and mouse cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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RA Babbage A.K., Bagguley C.L., Bailey J., Banerjee R., Barker D.J.,
RA Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.Y.,
RA Burford D.C., Burrill W., Burron J., Carder C., Carrer N.P.,
Chapman J.C., Clark S.Y., Clark G., Clee C.M., Clegg S., Cobley V.,
RA Collier R.E., Collins J.E., Colman L.K., Corby NR., Coville G.J.,
RA Collier K.M., Dhami P., Davies G., Clee C.M., Clegg S., Cobley V.,
RA Culley K.M., Dhami P., Davies G.J., Dunn M., Earthrowi M.E.,
B. Ellington A.E., Evans K.A., Faulkner L.K., Corby NR., Coville G.J.,
RA Gilby L.M., Gilson C.J., Glarner P., Garnett J., Ghori M.J.,
RA Gilby L.M., Gilson C.J., Gliffiths M.N.D., Halls K., Halls K.S.,
RA Hammond S.J., Howden P.J., Howe E., Heath D.D., Heathcott R.,
Andlines S.J., Howden P.J., Howe R.L., Howell G.R., Huckle E.,
RA Humphray S.J., Humphries M.D., Hult A.R., Johnson C.M., Joby A.A.,
Lawlor S., Leongamornlert D.A., Levershi M., Lloyd C.R., Lloyd D.M.,
RA Maslen G.L., Matthews L., McCarn O.T., McLiard G.K., Lloyd B.,
RA Mathews L., Moern-Jarry B.K., Parker A., Paete R.,
RA Pearce A.V., Peck A.I., Phillikin J.C., Niblett D., Nickerson T.,
RA Pearce A.V., Peck A.I., Phillikin J.C., Niblett D., Nickerson T.,
RA Squares S.L., Steward C.A., Sauth R., Smith M., Spraggon L.,
RA Whittaker H., Walls D.W., Thorpe A., Tracey A., Tromans A., Tubby B.,
RA Whittaker H., Wild A., Willey D.J., White S.S., Whittehead S.L.,
Ryatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
Ryatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A.,
Ryatt J.C., Young L., Younger R.M., Bentley D.R., Coulson A., Britan, B., Burther, B., Burt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! - FUNCTION: Involved in the presentation of foreign antigens to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immune system.
-!- SUBUNIT: Heterodimer of an alpha chain and a beta chain {beta-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             microglobulin).
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EMBL; X17093; CAA34947.1; -. HLA class I histocompatibility antigen, MIN, 14110; -
MIN, 14110; --Extracellular alpha-1. Extracellular alpha-2. Extracellular alpha-3. alpha chain F. EMBL; AF055066; AAC24827.1; -EMBL; AP000521; BAB63337.1; -EMBL; AL022723; CAB46623.1; -PIR; A60384; A60384.
HSSP; Q29961; 1HSA.
Genew; HGNC:4963; HLA-F. DOMAIN DOMAIN

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156
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                                                                                                                                                                                                                                                              140 DGKDYISLNEDLRSWTAADTVAQITQRFYBAEBYABEBFRTYLEGECLELLRRYLENGKET 199
                                                                                                                                                                                                                                                                                                 157 LORADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAG 215
                                                                                                                                                                                                                                                                                                                   200 LQRADPPKAHVAHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAG 258
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MEDLINE=22709134; PubMed=12799463;
Anzai T., Shina T., Kimura N., Yanagiya K., Kohara S., Shigenari A., Yamagata T., Kulski J.K., Naruse T.K., Fujimori Y., Fukuzumi Y., Yamagata T., Kulski J.K., Iwamoto C., Umehara Y., Imanishi T., Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H.;
"Comparative sequencing of human and chimparse MHC class I regions
                                                                                                                                                                                                 0; Gaps
                                              By similarity.
By similarity.
N-linked (GlCNAc. . .) (By similarity).
S -> P (in dbSNP:1736924).
/FIId-VAR_018327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                             55.3%; Score 119; DB 1; Length 362; 100.0%; Pred. No. 6.5e-117; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unveils insertions/deletions as the major path to genomic
                                                                                                                 /FTId=VAR 018327.
362 AA; 40568 MW; B8DD041F820A34E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 AA; 40625 MW; BA5699D08181A1FF CRC64;
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BOME: ABLOOMST, BACTB191.1; -

BOME: ABLOOMST, BACTB191.1; -

BOME: ABLOOMST, BACTB191.1; -

GO; GO: OOIGOSDS; P: C: integral to membrane; IEA.

GO; GO: OOIGOSSS; P: immune response; IEA.

InterPro: IPRO0110; Ig-like.

InterPro: IPRO01309; Ig-NHC.

InterPro: IPRO01309; Ig-NHC.

InterPro: IPRO01309; MHC_I.

InterPro: IPRO1059; MHC_I.

Pfam; PFO7554; C1-set; 1.

Pfam; PFO7554; C1-set; 1.

Pfam; PFO6623; MHC_I.

Pfam; PFO6623; MHC_I.

PFAM; SMO0407; IG-II.

PROSITE; PSSO835; IG-IKE; 1.

PROSITE; PSSO835; IG-IKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 Connecting peptide.
                              Cytoplasmic tail.
                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. v...
Anservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 362 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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2296
1220
1222
1224
107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Patr-F;
                                              DISULFID
DISULFID
CARBOHYD
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                                                                                                                                SEQUENCE
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                RANSMEM
                                                                                               VARIANT
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 DOMAIN
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Q7YR27
 SPIPI
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SEQUENCE FROM N.A. TISSUE-Lung;
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SEQUENCE
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Q860R0
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MEDLINE-22388257, PubMed=12477932,

MEDLINE-22388257, PubMed=12477932,

MISTAGE R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A platchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Galbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rheeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 DGKDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKET 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 DGKDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKET 199
157 LORADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAG 215
                                             200 LORADPPKAHVAHHPISDHEATLRCWALGFYPABITLIWORDGEBOTODTELVETRPAG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 LORADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 LQRADPPRAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRFAG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shiina T., Ota M., Katsuyama Y., Hashimoto N., Inoko H., "Genome diversity in HLA: A new strategy for detection of genetic polymorphisms in expressed genes within the HLA class III and class I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Butheria; Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 55.3%; Score 119; DB 2; Length 362; Best Local Similarity 100.0%; Pred. No. 6.5e-117; Matches 119; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regions.";
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AB088082; BAC54915.1; -.
SEQUENCE 362 AA; 40568 MW; B8DD041F820A34E1 CRC64;
                                                                                                                                                                                                        BACS4915;
02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
Major histocompatibility complex, class I, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY; PRT; 460 AA.,
                                                                                                                                                                   PRT; 362 AA.
                                                                                                          HLA-F protein (Fragment).
                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
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                                                                                                                                                                                    BAC54915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 DGKDYISLNEDLRSWIAADIVAQIIQRFYEAEEYAEEFRIYLEGECLELLRRYLENGKEI 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 LQRADPPKAHVAHHDISDHEATLRCWALGFYPABITLIWQRDGEBQTQDTELVETRPAG 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 LORADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAG 215
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
"Generation and infitial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.3%; Score 119; DB 2; Length 460; 100.0%; Pred. No. 8.1e-117; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 44.2%; Score 95; DB 2; Length 254. Best Local Similarity 100.0%; Pred. No. 1.2e-91; Matches 95; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu Y., He X., Xu.L., Zeng Y.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY255271; AAO86775.1;
GO; GO:0016020; C:membrane; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPRO01039; MHC_I:
PRINTS: RR01639; MHC_I: 1.
PRINTS: RR01639; MHC_I: 1.
PRODM; PRO00050; MHC_I: 1.
SEQUENCE 254 AA; 28588 MW; C81F225D409AAED2 CRC64;
                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (UTN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO09260; AAH09260.2; -.
HSSP; Q29961; 1HSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      460 AA; 52263 MW; C1A0B6891978D93E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 -(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                     GO, GO: 0016020; C: membrane, IEA.

GO, GO: 0016020; C: membrane, IEA.

GO, GO: 0006955; P: immune response; IEA.

InterPro; IPR00310; Ig_11ke.

InterPro; IPR003109; Ig_c1.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR001039; MHC_I.

Pfam; PF00129; MHC_I.

PRINTS; PR01638; MHC_I.

PRDDCM; PR01638; MHC_I.

SMART; SM01638; MHC_I.

SMART; SM01639; MHC_I.

SMART; SM01639; MHC_I.

SMART; SM01639; IG_IKE; I.

PROSITE; PS50835; IG_IKE; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.0 es 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MHC class Ib antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 LLRRYLENGKETLQRADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 ILRRYLENGKETLQRADPPKAHVAHHPISDHEATLRCWALGFYPABITLTWQRDGEEQTQ 161
44 IAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYWEWTTGYAKANAQTDRVALRNLL 103
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,

Tushiro H., Yamazaki M., Romiyama M., Sugiyama T., Irie R.,

Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,

Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,

Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,

Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,

Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ43284 fis, alone LYMPE2000083, highly similar to HLA CLASS I
HISTOCOMPATIBLLITY ANTIGEN, ALPHA CHAIN F.
                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                    y Match 33.0%; Score 71; DB 2; Length 349; Local Similarity 100.0%; Pred. No. 4.1e-66; hes 71; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349 AA; 39039 MW; 5C00196F03393AA1 CRC64;
                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FLJ43284.
Homo sapiens (Human).
                                        104 RRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHA 138
                           61 RRYNOSEAGSHTLOGMNGCDMGPDGRLLRGYHQHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 349 AA.
                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 DIELVETRPAG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 DTELVETRPAG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane
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BAC86108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                        Q6ZUW0
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                                                                                             RESULT 14
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BAC86108
                                                                                                          QEZUWO
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RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujianci Y., Komiyama M., Sugiyama T., Itie R.,
RA Kawai-Hio Y., Saito H., Wakamatsu M., Ishii S., Yamanoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Nagahari K., Masuho Y., Nagai K.,
RA Kawakami B., Suzuki Y., Jagano S., Nagahari K., Masuho Y., Nagai K.,
RY INDO human CDNA sequencing project.";
RY Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

SQ ENGUENCE 349 AA; 39039 MW; SCO0196F03393AA1 CRC64;

Query Match

A LASZ14; BAC86108:1;
Best Local Similarity 100.0%; Pred. No. 4:1e-66; Indels 0; Gaps

ON 145 LLRRYLENGKETLGRADPPKAHVAHHPISDHEATLRCWALGFYPABITLTWQRDGEEOTO 204

ON 162 LLRRYLENGKETLGRADPPKAHVAHHPISDHEATLRCWALGFYPABITLTWQRDGEEOTO 161

OY 205 DTELVETRPAG 215

Db 162 DTELVETRPAG 215

Search completed: December 15, 2004, 18:24:23

Search completed: December 15, 2004, 18:24:23
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

December 15, 2004, 18:13:46 ; Search time 21.9836 Seconds (without alignments) 941.000 Million cell updates/sec Run on:

1 IAVEYVDDTQFLRFDSDAAI.....QRDGBEQTQDTELVETRPAG 215 US-09-819-371-6 215 Title: Perfect score: Sequence:

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 0 Word size :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

.3 36
2.6
1.9 34
0.0
.2 36
4.9 25
.9 27
4.9 27
27
4.9 30
4.9 30
.9 33
.9 33
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4.9 35
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35
14.9 354
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35
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35
.95

MHC class I histoc	class I histocompa	class I histocompa	class I histocompa	MHC class 1 protei	HLA-B*5401 - human	transmembrane glyc	MHC HLA-B cell sur	HLA-B alpha-chain	HLA-B protein alph	gene HLA B-1519 pr	MHC class I histoc	lymphocyte antigen			
154418	HLHU40	HLHUB2	HLHUB7	JH0541	JH0539	JH0540	136962	156130	I84486	I62042	137492	S52486	138421	C35997	156149
6	Н	Н	Н	N	N	~	7	7	7	(7)	~	N	~1	~	01
361	362	362	362	362	362	362	362	362	362	362	362	362	362	362	362
14.9	14.9	14.9	14.9	14.9	14.9	14.9	14.9	14.9	14.9	14.9	14.9	14.9	14.9	14.9	14.9
32	32	32	35	32	32		32	35	32	32	32	32	32	32	32
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

MHC class I histocompatibility antigen HLA-F alpha chain Dew3 precursor - human C;Species: Homo sapiens (man) C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004 C;Accession: A60384; JUDIANO C;Accession: A60384; JUDIANO C;Accession: A60384; JUDIANO C; Epstein, H.; Holmes, N. Int. Immunol. 2, 531-537, 1990
A;Title: The buman class I MHC gene HLA-F is expressed in lymphocytes. A;Reference number: A60384; MUID:91197889; PMID:1707659

A; Molecule type: DNA A; Residues: L-362 cLUNA A; Cross-references: UNIPROT.P30511 B; Geraghty, D.E.; Wei, X.; Orr, H.T.; Koller, B.H. D. Exp. Med. 117, 1-18, 1990 A; Telle: Human leukocyte antigen F (HLA-F): an expressed HLA gene composed of a class I A; Reference number: JL0147; MUID:90111605; PMID:1688605

A, Molecule type: DNA A; Accession: JL0147

A;Residues: 1-362 <GER>
A;Cross-references: GB:X17093; NID:g32223; PIDN:CAA34947.1; PID:g312407
A;Experimental source: lymphoblastoid cell line C; Genetics:

A; Gene: GDB: HLA-F

A/Gene: Dosing.

A/Gene: Dosing.

A/Anthono: 6p21.3-6p21.3

A/Map position: 6p21.3-6p21.3

A/Anthono: 22/1 | 112/1, 204/1; 296/1; 335/1; 346/1; 362/1

C.Superfamily: class I histocompatibility antigen; immunoglobulin homology C.Keywords: glycoprofein; heterodimer; transmembrane protein

F.12-2.111/Domain: signal sequence #status predicted <SIG>
F.12-2.111/Domain: alpha-1 <ALI>
F.78-104/Region: hypervariable

F.112-203/Domain: alpha-2 <AL2>
F.154-4-295/Region: hypervariable

F.204-295/Domain: alpha-3 <AL2>
F.204-295/Domain: alpha-3 <AL3>
F.204-295/Domain: almunoglobulin homology <IMM>
F.207-282/Domain: almunoglobulin homology clown>
F.207-282/Domain: almunoglobulin homology clown>

0; Gaps Query Match 55.3%; Score 119; DB 2; Length 362; Best Local Similarity 100.0%; Pred. No. 7.8e-120; Matches 119; Conservative 0; Mismatches 0; Indels

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97 DGKDYISLNEDLRSWTAADTVAQITQRFYEAEERTATEGECLELLRRYLENGKET 156 140 DGKDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKET 199 g ઠે

157 LORADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAG 215 200 LQRADPPXAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAG 258 à qq

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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
A;Gene: GDB:HLA-C
A;Cross-references: GDB:119311; OMIM:142840
                                                                                                                                                               Query Match
Best Local Similarity 100.0
Matches 43, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
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A; Accession: JH0543
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Matches
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 14-Reb-1922 #sequence_revision 30-Jan-1993 #text_change 09-Jul-2004
C;Accession: C37028
R;Cianetti, L.; Testa, U.; Scotto, L.; La Valle, R.; Simeone, A.; Boccoli, G.; Giannella Immunogenetics 29, 80-91, 1989
A;Title: Three new class I HLA alleles: structure of mRNAs and alternative mechanisms of A;Reference number: A37028, MUID:89122144; PMID:2914713
A;Accession: C37028
A;Scatus: preliminary
A;Molecule type: mRNA
A;Residues: 1-316 <CIA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPROT:P33617; EMBL:Z21819; NID:g38568; PIDN:CAA79885.1; PID:g38569
C,Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q96FQ5; UNIPROT:Q9987; UNIPROT:Q9M34; UNIPROT:O19677; UNIA
                                                                                                          C. Accession: S0114
R. Lawlor, D.A.; Ward, F.E.; Ennis, P.D.; Jackson, A.P.; Parham, P.
Nature 335, 268-271, 1988
A. Title: HLA-A and B polymorphisms predate the divergence of humans and chimpanzees.
A.; Reference number: S06424; MUID:88319000; PMID:3412487
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                        4C class I histocompatibility antigen Ch28 alpha chain precursor - chimpanzee, Species: Pan troglodytes (chimpanzee) Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 DGKDYISLNEDLRSWTAADTVAQITQRFYEABEYAEEFRTYLEGECLELLRRYLENGKET 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 DGKDYISINEDI.RSWTAADTVAQITQRFYEAEBYAEBFRTYLEGECLELLRRYLENGKET 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          histocompatibility antigen, HLA-F-like - rhesus macaque
CiSpecies: Macaca mulatta (rhesus macaque)
Cipate: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
CiAccession: 82999
R;Bontrop, R.R.
R;Bontrop, R.R.
A;Reference number: 829990
A;Reference number: 829990
                                                                                                                                                                                                                                                                                                                  A,Molecule type: mRNA

A,Molecule type: mRNA

Residues: 1-345 <LAM>

C,Superfamily: class I histocompatibility antigen; immunoglobulin homology

C,Reywords: glycoprotein; membrane protein

F,217-282/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165 ITQRFYEAEBYAEEFRTYLEGECLELLRRYLENGKETLQRADPPKAH 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 345;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.6%; Score 70; DB 2; Le
ilarity 100.0%; Pred. No. 4.3e-67;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 LORADPPKAH 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 LORADPPKAH 209
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                                                                                                                                                                                                                                                                   A; Accession: S07114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Cises I histocompatibility antigen heavy chain precursor - lowland gorilla
Cispecies: Gorilla gorilla (lowland gorilla)
Cispecies: Gorilla gorilla gorilla (lowland gorilla)
Cispecies: Gorilla gorilla gorilla (lowland gorilla)
Ciscocasion: JROS44; JHOS43
Rilawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
Rilawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
A; Title: Gorilla class I major histocompatibility complex alleles: comparison to human ar A; Reference number: JHOS34; MUID:92078860; PMID:1744581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C;Dates: 02-Jul-1996 #sequence_revision 02-Jul-1999
R;Choo, S: Y: Starling, G:C: Anasetti, C: Hansen, J.A.
Hum. Immunol. 36, 20-26, 1993
A;Title: Salection of an unrelated donor for marrow transplantation facilitated by the m. A;Reference number: 154307; WUID:93209813; PMID:8458735
A;Accession: 154307
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C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
Ksywords: transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-365/Product: class I histocompatibility antigen heavy chain #status predicted <CLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A)Residues: 1-365 <LAW>
A)Cross-references: UNIPROT:P30383; EMBL:X60250; NID:g22878; PIDN:CAA42802.1; PID:g22879
A)Experimental source: EBV-transformed B cell
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A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;170-235/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the authors translated the codon AGT for residue 320 as Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.2%; Score 37; DB 2; Length 365; 100.0%; Pred. No. 1.5e-31; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                         173 SDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAG 215
                                                                                                                                                                                                                                                                                                                                                                                           169 SDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAG 211
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F;207-298/Domain: alpha-3 <AL3>
F;220-285/Domain: immunoglobulin homology <IMM>
F;229-365/Domain: intracellular #status predicted <INT>
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                                                                                                                                                                  20.0%; Score 43; DB 2; Le
100.0%; Pred. No. 4.6e-38;
iive 0; Mismatches 0;
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A,Readidues: 1-319, (%,321-365 <1A2>
A)CTOSB-references: EMBL:X60252
A)Experimental source: EBV-transformed B cell
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C;Accession: S24439

R;Warkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garbe Nature 357, 329-333, 1992
Asture 357, 329-333, 1992
A;Title: New recombinant HIA-B alleles in a tribe of South American Amerindians indicate A;Reference number: S24027; MUID:92269956; PMID:1589035
                                                                                                                                                                                                                     A; Accession: $24439
A; Molecule type: mRNA
A; Residues: 1-274 < WAT>
A; Residues: 1-274 < WAT>
A; Cross-references: UNIPROT: Q96DW9; UNIPROT: Q8WLS2; UNIPROT: O19790; UNIPROT: Q95351; UNIPPOT: O78218; UNIPROF: (229653; UNIPROT: Q29654; UNIPROF: Q29655; UNIPROT: Q29655; UNIPROT: Q095346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Keywords: glycoprotein
C; L-90/Domain: alpha-1 #status predicted <EXL>
F; 91-182/Domain: alpha-1 #status predicted <EXL>
F; 91-261/Domain: impunoglobulin homology <IMA>
F; 96-261/Domain: impunoglobulin homology <IMA>
F; 96-261/Domain: impunoglobulin homology <IMA>
F; 96-86/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 101-164, 203-259/Disulfide bonds: #status predicted
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Nighternate names: MTC Chib chain.

Nighternate names: MTC Chib chain.

Cispecies: Pan troglodytes (chimpanzee)

Cispecies: Pan troglodytes (chimpanzee)

Cispecies: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004

Cispecies: 315, 13696

Cispecies: Nature 335, 268-271, 1988

Nithle: HhaA and B polymorphisms predate the divergence of humans and chimpanzees.

Alreference number: S06424; MUD: 88319000; PMID: 3412487
           C,Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
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C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Reywords: glycoprotein; membrane protein
F; Reywords: glycoprotein; membrane protein
F; SB-149/Domain: alpha-2 #status predicted <EX2>
F; 163-228/Domain: immunoglobulin homology <IMM>
F; 250-274/Domain: immunoglobulin homology <IMM>
F; 250-274/Domain: intraorellular #status predicted <INM>
F; 275-305/Domain: intraorellular #status predicted <INT>
F; S3/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 68-131,170-226/Disulfide bonds: #status predicted
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R;Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
J. Immunol. 142, 3937-3950, 1989
A;Title: Diversity and diversification of HLA-A,B,C alleles.
A;Reference number: 136956; MUID:89235215; PMID:2715640
A;Accession: 136960
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100.0%; Pred. No. ...
... 0; Mismatches
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14.9%; Score 32; DB 3
Best Local Similarity 100.0%; Pred. No. 3.16
Matches 32; Conservative 0; Mismatches
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Matches 32; Conservative
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A; Residues: 1-305 < LAW>
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A; Residues: 1-305 <RES>
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C;Species: Homo sapiens (man)
C;Date: O'~unn-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: 154463
R;Mueller, C.A.; Engler-Blum, G.; Gekeler, V.; Steiert, I.; Weiss, E.; Schmidt, H.
Immunogenetics 30, 200-207, 1989
A;Title: Genetic and serological heterogeneity of the supertypic HLA-B locus specificiti
A;Reference number: 154463; MUID:89379286; PMID:2777338
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A,Residues: 1-274 «RES.
A,Cross-references: UNIPROT:Q95365; GB:M29864; NID:g187674; PIDN:AAA36222.1; PID:g187675
C,Superfamily: class I histocompatiblity antigen; immunoglobulin homology
F;196-261/Domain: immunoglobulin homology <IMM>
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A;Crose-references: UNIPROT:029937; GB:M29865; NID:g187676; PIDN:AAA36223.1; PID:g187677
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
P;196-261/Domain: immunoglobulin homology <IVM>
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A,Reference number: 154463; WUID:89379286; PMID:2777338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Mueller, C.A.; Engler-Blum, G.; Gekeler, V.; Stelert, I.; Weiss, E.; Schmidt, H. Immunogenetics 30, 200-207, 1989
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. Species: Homo sapiens (man)
.Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
.Accession: I68774
A, Residues: 1-255 <RES>
A, Cross-references: GB:M93657; NID:g184155; PIDN:AAA58650.1; PID:g553335. C; Genetics: A, Gene: HLA-A30JS
C, Superfamily: class I histocompatibility antigen; immunoglobulin homology
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1 Similarity 100.0%; Pred. No. 2.7e-26;
32; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Status: preliminary; translated from GB/EMBL/DDBJA; Molecule type: DNA
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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ilarity 100.0%; Pred. No. 2.8
Conservative 0; Mismatches
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Best Local Similarity
Matches 32; Conserv
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Best Local Similarity
Matches 32, Conserv
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RESULT 8

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C)Accession: 166747

E)Accession: 166747

MulDispose and the evolution of the HLA-B a. A;Reference number: 15457; MULD: 89233295; PMID: 2714852

A;Reference number: 154457; MULD: 89233295; PMID: 2714852

A;Accession: 166747

A;Accession: 16
                                          C;Accession: I56116

F;Choo, S.Y.; Fan, L.A.; Hansen, J.A.

J. Immunol. 147, 174-180, 1991

A;Title: A novel HIA-B27 allele maps B27 allospecificity to the region around position 70

A;Reference number: I56116, MUID:91268545; PMID:1711072

A;Accession: I56116

A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross_references: UNIPROT:P03989; GB:M62852; NID:g187760; PIDN:AAAS9647.1; PID:g187761
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;196-261/Domain: immunoglobulin homology <IMM>
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A, Residues: 1-350 <RES>
A, Cross-references: University of SE.M28204; NID:9576472; PIDN:AAA53257.1; PID:9576473
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
F; 208-273/Pomain: immunoglobulin homology <IWM>
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross_references: UNIPROT:Q08173; GB:L07950; NID:g307236; PIDN:AAAS9683.1; PID:g307237
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R;Rodriguez, S.G.; Johnson, A.H.; Hurley, C.K.
Hw. Immunol. 37, 192-194, 1993
A;Title: Molecular characterization of HLA-B71 from an African American individual. A;Reference number: 154308; MUID:94064392; PMID:8244782
A;Accession: 154308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IS4308
MC HIA B71 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: O2-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
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C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C,Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
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A;Map position: 6201.3-6621.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
P;220-285/Pomain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.9%; Score 32; DB 2; Length 338; 100.0%; Pred. No. 3.4e-26; ive 0; Mismatches 0; Indels
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Best Local Similarity 100.0
Matches 32; Conservative
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Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-338 < RES>
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A;Cross-references: UNFOT:019357; GB:M24044; NID:g176812; PIDN:AAA35423.1; PID:g176813
S;Cyogrfamily: class I histocompatibility antigen; immunoglobulin homology
F;166-231/Domain: immunoglobulin homology <IMM>
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                                                                      MIC Chi.A chain - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
C;Species: Pan troglodytes (chimpanzee)
C;Accession: 136556
R;Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
J;Immunol: 142, 337-3950, 1989
A;Title: Diversity and diversification of HLA-A, B,C alleles.
A;Reference number: 136956, MUID:89235215; PMID:2715640
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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A.Residues: 1-312 <RES>
A.Residues: 1-312 <RES>
A.Cross-references: GB.M24047, NID:g176818; PIDN:AAA35426.1; PID:g553155
A.Cross-references: GB.M24047, NID:g176818; PIDN:AAA35426.1; PID:g553155
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: glycoprotein; membrane protein
F:1240-Momain: alpha-1 #status predicted <RIS-
F:125-114/Domain: alpha-1 #status predicted <RX>
F:125-114/Domain: alpha-2 #status predicted <RX>
F:120-285/Domain: immunoglobulin homology <IRM>
F:120-285/Domain: transmembrane #status predicted <IVM>
F:1070-131/Omain: cransmembrane #status predicted <IVM>
F:110/Plinding site: carbohydrate (Aan) (covalent) #status predicted
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Title: Diversity and diversification of HLA-A,B,C alleles.; Reference number: 136956; MUID:89235215; PMID:2715640
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Residues: 1-332 <LAW>
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Gaps

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14.9%; Score 32; DB 2; Length 350;
  Query Match
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MHC HLA-B27-HS - human (fragment) C; Species: Homo sapiens (man)

ó 0; Gaps Best Local Similarity 100.0%; Pred. No. 3.6e-26; Matches 32; Conservative 0; Mismatches 0; Indels

169 HHPISDHEATLRCWALGFYPAEITLTWQRDGE 200

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Search completed: December 15, 2004, 18:25:18 Job time: 22.9836 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Published Applications AA:*

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Sequence 6, Appli Sequence 1411, Ap Sequence 5, Appli Sequence 82, Appli Sequence 1887, Ap Sequence 30718, Ap Sequence 30718, Ap Sequence 3541, Appli Sequence 799, App Sequence 799, App Sequence 799, App Description 1. US-09-819-371-6 1. US-09-925-301-1431 1. US-09-919-371-5 1. US-09-919-371-8 1. US-09-919-371-4 1. US-09-919-371-4 1. US-09-936-30718 1. US-09-84-761-35461 1. US-09-96-692-2139 1. US-09-796-692-2139 1. US-10-040-862-2139 1. US-10-040-862-2139 1. US-10-040-862-2139 SUMMARIES 111 114 114 114 141 141 141 Query Match Length DB Score Result

Sequence 799, App Sequence 213, Ap Sequence 213, App Sequence 799, App Sequence 799, App Sequence 3505, App Sequence 3505, App Sequence 3505, App Sequence 355, App Sequence 155, Appl Sequence 155, Appl Sequence 16, Appl Sequence 216, Appl Sequence 217, Appl Sequence 217, Appl Sequence 217, Appl Sequence 33990, Sequence 217, Appl Sequence 314, Appl Sequence 32, Appl Sequence 34, Appl Sequence 34, Appl Sequence 3805, Appl	Sequence 380, App Sequence 388, App
15 US-10-057-4758-799 15 US-10-057-4758-799 15 US-10-154-8848-2139 16 US-10-154-8848-2139 16 US-10-154-8848-2139 16 US-10-764-324-799 17 US-10-764-324-799 18 US-10-262-339-48 19 US-09-925-302-835 10 US-09-925-302-835 11 US-10-264-049-3505 12 US-10-209-386-31089 17 US-10-029-386-316 17 US-10-029-386-317 18 US-10-029-386-329 19 US-09-884-15-115-363890 9 US-09-884-172-21 10 US-09-884-15-115-363890 9 US-09-884-172-21 10 US-09-884-172-21 11 US-10-172-115-363890 9 US-09-884-172-21 15 US-10-1380-889-32 15 US-10-380-889-32 16 US-10-380-889-32 17 US-10-380-889-32 18 US-10-380-889-32 19 US-09-8810-560-8 16 US-10-380-889-38-38-38-38-38-38-38-38-38-38-38-38-38-	
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ALIGNMENTS

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Sequence 6, Application US/09819371
| Publication No. US200400533441
| GENERAL INFORMATION:
| APPLICANT: Egawa, Kohjt | TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can | TITLE OF INVENTION: Using Thereof | FILE REPERENCE: 30815 | CURRENT APPLICATION NUMBER: US/09/819,371 | CURRENT FILING DETER: 2002-03-15 | NUMBER OF SEQ ID NOS: 6 | SOFTWARE: Patentin Version 3.0 | SEQ ID NO 6 | SE
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CORGANISM: Homo sapiens
US-09-819-371-6
US-09-819-371-6
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97 DGKDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKET 156
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APPLICANT: Zhang, Bing
APPLICANT: Glan, Bradford W.
APPLICANT: Glan, Gary M.
APPLICANT: Glan, Gary M.
APPLICANT: Glan, Gary M.
TITLE OF INVENTION: TRREAFE E.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTECME
TITLE OF INVENTION: 10ENTIFIED IN THE MITOCHONDRIAL PROTECME
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT PILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FRANKE FRANKE (FRANKE)
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SOFTWARE (
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                                                                                                      APPLICANT: Morin, Patrice J.
APPLICANT: Sherman-Baust, Cheryl A.
APPLICANT: Sherman-Baust, Cheryl A.
APPLICANT: Fizer, Ellen S.
APPLICANT: Pizer, Ellen S.
APPLICANT: Hough, Colleen D.
TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER.
FILE RERERENCE: 14014, 036912
CURRENT APPLICATION NUMBER: US/10/257,021
CURRENT FILING DATE: 2002-10-03
PRIOR PELICATION NUMBER: 60/194,336
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-03
PRIOR FILING DATE: 2001-04-03
NUMBER OF SEQ ID NOS: 147
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 82.
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Best Local Similarity 100.0%; Pred. No. 2.5e-108;
Matches 119; Conservative 0; Mismatches 0;
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Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Eoin D.
Sequence 82, Application US/10257021 Publication No. US20030211498A1 GENERAL INFORMATION:
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Best Local Similarity 100.(
Matches 119; Conservative
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CORGANISM: Homo sapiens
US-10-408-765A-1887
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CRGANISM: Homo sapiens
US-10-257-021-82
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TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Car
TITLE OF INVENTION: Using Thereof
FILE REPERRNCE: 30815
CURRENT APPLICATION NUMBER: US/09/819,371
CURRENT FILE BET STORE STORE STORE SOOZ-03-15
SOFTWARE FILE DE NOS: 6
SOFTWARE: Patentin version 3.0
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APPLICANT: ROSEN et al.

TITILE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REPERENCE: PALO

CURRENT APPLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR PLING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOOTMARE: PatentIN Ver. 2.0
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181 CWALGFYPAEITLIWQRDGEEQTQDTELVETRPAG 215
                                                                                                                                                                                                                                       Sequence 1431, Application US/09925301 Patent No. US20020052308A1
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, Sequence 5. Application US/09819371
; Publication No. US20040053344A1
; GENERAL INFORMATION:
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US-09-925-301-1431
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US-10-257-021-82
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Query Match 24.2%; Score 52; DB 15; Length 186; Best Local Similarity 100.0%; Pred. No. 1.1e-42; Matches 52; Conservative 0; Mismatches 0; Indels
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                                                                                                    APPLICANT: Egawa, Kohji
TITIE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Car
TITIE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Car
FILE REFERENCE: 30815
CURRENT APPLICATION NUMBER: US/09/819,371
CURRENT PILING DATE: 2002-03-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.0
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Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, David R.
APPLICANT: HUXAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR CITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REPRENCE: ACOUNTICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
NUMBER: OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 30718
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CTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6
CHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12
CTHER INFORMATION: SWISSPROT HIT: P30511, EVALUE 2.00e-52
US-10-029-386-30718
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                              Sequence 4, Application US/09819371
Publication No. US20040053344A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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US-10-029-386-30718
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US-10-264-049-4063
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US-09-819-371-4
                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 4
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LOCATION: (86). OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (124)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (174)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     j LOCATION: (180)
j: OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
VS-10-264-049-4063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L-amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (77) OTHER INFORMATION: Xaa equals any of the twenty naturally occurring PRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MISC FEATURE
LOCATION: (148)
OTHER INFORMATION: Xaa equals any of the twenty naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               equals any of the twenty naturally occurring
HILL OF INVENTION: Nucleic Acids, Proteins, and Antibodies;
FILE REPERENCE: PA13391
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT PILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR PILING DATE: 2001-06-07
PRIOR PILING DATE: 2000-06-07
PRIOR PILING DATE: 2000-06-07
NUMBER: OF SEQ ID NOS: 4360
SOFTWARE: Patentin Ver. 3.1
SEQ ID NO 4063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MISC FEATURE LOCATION: (123)
OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MISC_FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: MISC_FEATURE
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Gaps

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GENERAL INTORMATION:
APPLICANT: Algate, Paul A.
APPLICANT: Adminion, Jane
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
CURRENT PILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190, 479
PRIOR APPLICATION NUMBER: 60/200, 545
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-06-07-04
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-06-03
PRIOR PILING DATE: 2000-06-04
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) OTHER INFORMATION: EST HUMAN HIT: AW820291.1, EVALUE 3.00e-52; OTHER INFORMATION: SWISSPROT HIT: P30487, EVALUE 3.00e-53 US-09-864-761-35461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 14.9%; Score 32; DB 9; Length 110; Best Local Similarity 100.0%; Pred. No. 3e<sub>7</sub>23; Matches 32; Conservative 0; Mismatches 0; Indels
                                                                                                                                                Length 91;
                                                                                                                                                                                                                            0; Indels
                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 2.6e-23;
Matches 32; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 HHPISDHEATLRCWALGFYPAEITLTWORDGE 200
                                                                                                                                                                                                                                                                                                169 HHPISDHEATLRCWALGFYPAEITLTWORDGE 200
                                                                                                                                                                                                                                                                                                                                        8 HHPISDHEATLRCWALGFYPABITLTWQRDGE 39
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SOFTWARE FRAESEQ for Windows Version 3.0
SEQ ID NO 799
LENGTH: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 2139, Application US/09796692; Publication No. US20020198362A1
GAPBEAL INFORMATION:
APPLICANT: Gaiger, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 799, Application US/09796692
Publication No. US20020198362A1
GENERAL INFORMATION:
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US-09-796-692-799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-796-692-2139
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US-09-796-692-799
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PREMEAL. INTERGRATION.

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.
                                                1 YAKANAQTDRVALRNILIRRYNQSEAGSHTLQGWNGCDMGPDGRLLRGYHQHA 52
        44 YAKANAQIDRVALRNLLRRYNQSEAGSHILQGMNGCDMGPDGRLLRGYHQHA 95
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 24

OTHER INFORMATION: EXPRESSED IN HELA. SIGNAL = 47

OTHER INFORMATION: EXPRESSED IN HELA. SIGNAL = 47

OTHER INFORMATION: EXPRESSED IN HERAT, SIGNAL = 17

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.7

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 32

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 58

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 15

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 15

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 15

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 15
                                                                                                                                                                                                                                                                Sequence 35461, Application US/09864761
Patent No. US20020048763A1
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                        RESULT 9
US-09-864-761-35461
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TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
TITLE OF INVENTION: Hematological Malignancies
CURRENT APPLICATION NUMBER: US/0/40,862
CURRENT FILING DATE: 2001-11-06
PRIOR PELICATION NUMBER: US 60/186,126
PRIOR PELICATION NUMBER: US 60/180,479
PRIOR PELICATION NUMBER: US 60/200,545
PRIOR PELICATION NUMBER: US 60/200,303
PRIOR APPLICATION NUMBER: US 60/200,709
PRIOR PELICATION NUMBER: US 60/200,709
PRIOR PELICATION NUMBER: US 60/200,999
PRIOR PELICATION NUMBER: US 60/200,999
PRIOR PELICATION NUMBER: US 60/200,999
PRIOR PELICATION NUMBER: US 60/202,084
PRIOR PELICATION NUMBER: US 60/202,084
PRIOR PELICATION NUMBER: US 60/202,903
PRIOR PELICATION NUMBER: US 60/202,903
PRIOR PELICATION NUMBER: US 60/202,903
PRIOR PELICATION NUMBER: US 60/202,316
PRIOR PELICATION NUMBER: US 60/203,318
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PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR PLICATION NUMBER: US 60/202,084
PRIOR PLING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR PLING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR PLING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
PRIOR PLING DATE: 2000-08-04
PRIOR PRIING DATE: 2000-08-04
PRIOR PLING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR PLING DATE: 2000-08-07
PRIOR PLING DATE: 2000-08-07
PRIOR PLING DATE: 2000-08-07
PRIOR PLING DATE: 2000-08-07
PRIOR PRING DATE: 2000-08-07
PRIOR PRIME PAPELICATION NUMBER: US 69/796,692
NUMBER OF SEQ ID NOS: 10467
SOFTHARE: FastSEQ for Windows Version 3.0
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Publication No. US20030078396A1
GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: COTAN COMPANION
THERE OF INFORMATION
THERE OF INFORMATION
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; ORGANISM: Homo sapiens
US-10-040-862-799
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Matches 32; Conserv
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                    APPLICANI: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: UNMERS: US/09/796,692
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT APPLICATION NUMBER: 06/186,126
PRIOR PELING DATE: 2000-03-01
PRIOR PELING DATE: 2000-03-01
PRIOR FILING DATE: 2000-04-28
PRIOR PELING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 66/200,303
PRIOR PELING DATE: 2000-04-28
PRIOR PELING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 66/200,999
PRIOR PELING DATE: 2000-05-01
PRIOR PELING DATE: 2000-06-01
PRIOR PELING DATE: 2000-06-01
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Sequence 799, Application US/10040862

Publication No. US20030078396A1

Sequence 799, Application US/10040862

Publication No. US20030078396A1

APPLICANT: Alexander

APPLICANT: Alexander

APPLICANT: Mannion, Jane

APPLICANT: Mannion, Jane

APPLICANT: Mannion, Jane

APPLICANT: Retter, Marc

APPLICANT: Corixa Corporation

ITILE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy

TITLE OF INVENTION: Hemacological Malignancies

FILE REFERENCE: 014058-0152005

CURRENT FILING DATE: 2001-11-06

PRIOR APPLICATION NUMBER: US 60/190, 479

PRIOR PILING DATE: 2000-04-28

PRIOR PLING DATE: 2000-04-28

PRIOR PILING DATE: 2000-04-28

PRIOR PILING DATE: 2000-04-28

PRIOR FILING DATE: 2000-04-28
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Best Local Similarity 100.0%; Pred. No. 3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels
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SOFTWARE: FastSEQ for Windows Version 3.0
        APPLICANT: Algate, Paul A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
) ORGANISM: Homo sapiens
US-09-796-692-2139
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APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Gaiger, Jonathan David
APPLICANT: Wang Aijun
APPLICANT: Ordonez, Nadia
APPLICANT: Ordonez, Nadia
APPLICANT: Carter, Lauren
APPLICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2002-01-22

PRIOR APPLICATION NUMBER: US 60/186,126

PRIOR APPLICATION NUMBER: US 60/186,126

PRIOR APPLICATION NUMBER: US 60/190,479

PRIOR PELLING DATE: 2000-03-17

PRIOR PELLING DATE: 2000-03-17

PRIOR PELLING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: US 60/200,303

PRIOR APPLICATION NUMBER: US 60/200,779

PRIOR APPLICATION NUMBER: US 60/200,999

PRIOR PELLING DATE: 2000-04-28

PRIOR PELLING DATE: 2000-05-04

PRIOR PELLING DATE: 2000-05-04

PRIOR PELLING DATE: 2000-05-04

PRIOR PELLING DATE: 2000-05-04

PRIOR PELLING DATE: 2000-05-22

PRIOR PELLING DATE: 2000-05-24

PRIOR APPLICATION NUMBER: US 60/222,903

PRIOR APPLICATION NUMBER: US 60/222,903

PRIOR PELLING DATE: 2000-07-14

PRIOR PELLING DATE: 2000-07-14
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                                                                                                                                                                                                                      Sequence 2139, Application US/10057475B Publication No. US20040002068A1 GENERAL INFORMATION:
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                                                                                                                 RESULT 15
US-10-057-475B-2139
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Sequence 799, Application US/10057475B

Publication No. US2004002068A1

SERVEAL INCRMATION:
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Jouathan David
APPLICANT: Manio, Jouathan David
APPLICANT: Clapper, Jouathan David
APPLICANT: Cargoer, Jouathan David
APPLICANT: Cargoer, Jouathan David
APPLICANT: Cargoer, Jouathan David
APPLICANT: Cargoer, Jauren
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SOFTWARE: FastSEQ for Windows Version 3.0
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14.9%; Score 32; DB 14; Length 110;
Best Local Similarity 100.0%; Pred. No. 3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels
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32; Conservative 0; Mismatches
PRIOR FILING DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FactSEQ for Windows Version 3.0
SEQ ID NO 2139
LENGTH: 110
TYPE: PRT
ORCANISM: PRT
US-10-040-862-2139
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GORGANISM: Homo sapiens
US-10-057-4758-799
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Sequence 9, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 22, Appli
Sequence 22, Appli
Sequence 22, Appli
Sequence 22, Appli
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                                                                               December 15, 2004, 18:14:01; Search time 24.182 Seconds (without alignments) 589.627 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-123-581-1
US-08-1406-057-9
US-08-96-057-9
US-08-96-316-9
US-08-96-316-9
US-08-96-316-9
US-08-95-3-444A-22
US-08-95-3-444A-22
US-08-95-3-444A-22
US-08-123-999-25
US-08-123-999-25
US-08-123-96-135
US-08-123-96-105
US-08-123-96-105
US-08-123-96-106
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US-08-123-96-106
US-08-123-96-107
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                                                      - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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Match Length
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| Sequence 4290, Application US/09513999C
| Patent No. 6783961
| GENERAL INFORMATION:
| APPLICANT: Dunds Milne Edwards, J.B.
| APPLICANT: Duclert, A.
| TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
| FILE REFERENCE: 59.US2.REG
| CURRENT APPLICATION NUMBER: US/09/513,999C
| CURRENT APPLICATION NUMBER: US 60/122,487
| FRIOR APPLICATION NUMBER: US 60/122,487
| FRIOR FILING DATE: 1999-02-26
| NUMBER OF SEQ ID NOS: 36681
| SOPTHARE: BEACH.PM
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Patent No. 5723128
GENERAL INFORMATION:
APPLICANT: CLAYBERGER, CAROL A.
APPLICANT: REENSKY, ALAN M.
APPLICANT: REENSKY, ALAN M.
APPLICANT: TORRINAM, PETER
TITLE OF INVENTION: CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")
            US-08-484-905-199
US-08-484-905-101
US-08-484-905-101
US-08-484-905-103
US-08-481-985B-99
US-08-481-985B-99
US-08-481-985B-100
US-08-481-985B-101
US-08-481-985B-103
US-08-652-23
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; OTHER INFORMATION: SCORE 9.3
; OTHER INFORMATION: Seq SLLLLLSGALALT/DT
US-09-513-999C-4290
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TYPE: PRT
ORGANISM: Homo sapiens
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US-09-513-999C-4290
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LENGTH: 120
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US-08-222-851-1
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US-09-153-586-21

| Sequence 21, Application US/09153586A |
| Patent No. 6270772 |
| GENERAL INFORMATION: |
| APPLICANT: BURTOWS et al. |
| TITLE OF INVENTION: antigen-specific T-Cells |
| TITLE OF INVENTION: antigen-specific T-Cells |
| TITLE OF INVENTION: antigen-specific T-Cells |
| TITLE OF INVENTION: ANTIGEN SPECIFIC T-CELS |
| FILE REFERENCE: 48823 |
| CURRENT APPLICATION NUMBER: 60/064,552 |
| EARLIER APPLICATION NUMBER: 60/064,555 |
| EARLIER PILING DATE: 1997-09-16 |
| EARLIER PILING DATE: 1997-10-10 |
| NUMBER OF SEQ ID NOS: 30 |
| NUMBER OF SEQ ID NOS: 30 |
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TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES NUMBER OF SEQUENCES: 43 CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESSEE: AD
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14.9%; Score 32; DB 1; Length 274;
Best Local Similarity 100.0%; Pred. No. 5.7e-24;
Matches 32; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.9e-09;
tive 0; Mismatches 0; Indels
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COUNTY: USA

ITE: 20016-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC LOSS/MS-DOS
SOFTWARE: PETENT PC-DOSS/MS-DOS
SOFTWARE: PETENT PC-DOSS/MS-DOS
SOFTWARE: PETENT PC-DOSS/MS-DOS
SOFTWARE: PETENT PC-DOSS/MS-DOS
SOFTWARE: PETENT PC-DOSS/MS-DOSS
FILING DATE: 05-APR-1994
CITASSIFICATION NUMBER: 36,217
REFERENCE/DOCKET NUMBER: 28600-20200.22
REPERENCE/DOCKET NUMBER: 28600-20200.22
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 28600-20200.22
TELECOMMUNICATION NUMBER: 28600-20200.22
TELECOMMUNICATION NUMBER: 38600-20200.22
TELECOMMUNICATION NUMBER: 28600-20200.22
TELECOMMUNICATION ON RESNICERESMEN
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH = Amino acide
TYPE: Amino acide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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; TOPOLOGY: linear
US-08-222-851-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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Matches 17; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-153-586-21
                                                                                                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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Gaps
         Sequence 9, Application US/08406057
Patent No. 585642
GENERAL INFORMATION:
APPLICANT: CAROSELLA, EDGARDO D
APPLICANT: MOREAU, PHILIPPE
APPLICANT: MCREAU, PHILIPPE
APPLICANT: MCREAU, PHILIPPE
APPLICANT: MCREAUN, MAREN
TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLOW, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 117;
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APPLICANT: CAROSELLA, EDGAEDO D
APPLICANT: CAROSELLA, EDGAEDO D
APPLICANT: GLUCKAGAN, ELIANE
APPLICANT: GLUCKAGAN, ELIANE
APPLICANT: KIRSZENBADA, MAREK
TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
ITLE OF INVENTION: GENE AND THEIR APPLICATIONS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR GITY: ARLINGTON STATE: VIGGINIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE
MEDIUM TYPE: Tape
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPACTION
CORPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,057
FILING DATE: 17-MAR-1995
FILING DATE: 17-MAR-1995
FILING DATE: 18-MAR-1994
FILING DATE: 18-MAR-1996
FILING DATE: 18
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7.4%; Score 16; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 2.6e-08;
Matches 16; Conservative 0; Mismatches 0;
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Patent No. 6291659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 EATLRCWALGFYPAEI 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 2202
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: peptide US-08-406-057-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-08-958-316-9
JS-08-406-057-9
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TOPOLOGY: linear
MOLECULE TYPE: peptide
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F: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR ARLINGNIA
VIRGUIA
XY: USA
                                                                                                                                                                                                                                                                       OPERAING SYSTEM: COMPACTORY
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/958,316
FILING DATE: 27-OCT-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 03179
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN FROSTATION OF RECIPEATION NUMBER: 0846-0437-0
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION ON 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TELENT TYPE: amino acids
TENTAMENT AND ACIDENT ACID
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MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,057
FILING DATE: 17-MAR-1995
CLASSIFICATION: 435
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APPLICATION NUMBER: FR 94 03179
                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 EATLRCWALGFYPAEI 191
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: peptide US-08-958-316-9
                                          CITY: AR
STATE: V
COUNTRY:
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ATTORNY GREW 18-WAS 1994

ATTORNY GREW 18-WAS 1994

RESISTANTON NUMBER: 34.618

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TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
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; Patent No. 6140305
; GENERAL INFORMATION:
; APPLICANT: Thomas;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                           Gaps
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OTHER INFORMATION: /note= "Rabbit leukocyte antigen (RLA)"
US-08-652-265-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
7.4%; Score 16; DB 3; Length 361;
Best Local Similarity 100.0%; Pred. No. 7.2e.08;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                MESULT 8
US-08-652-265-22
| Sequence 2.2. Application US/08652265
| Patent No. 6025130
| Patent No. 6025130
| Patent INFORMATION:
| APPLICANT: Thomas, Winston J. APPLICANT: Grain Designation of APPLICANT: Ruddy, David No. 84PLICANT: Ruddy, David No. 84PLICANT: Ruddy, David APPLICANT: Ruddy, David APPLICANT: Ruddy, David APPLICANT: Wolff, Roger K. TITLE OF INVENTION: Hereditary Hemochromatosis Gene NUMBER OF SEQUENCES: 44
| CORRESPONDENCE ADDRESS: ADDRESSE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Bighth Floor STATE: California
| COUNTRY: USA
                                       Query Match
7.4%; Score 16; DB 3; Length 145;
Best Local Similarity. 100.0%; Pred. No. 3.1e-08;
Matches 16; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,265
FILING DATE: 23-MAY-1996
CIASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: Smith, William M.
REGASTRATION NUMBER: 17957-000500
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94111-3834
COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                     176 EATLRCWALGFYPAEI 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176 EATLRCWALGFYPAEI 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-08-834-497A-22
US-08-958-316-8
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APPLICANT: Thomas winston J.
APPLICANT: Thomas winston J.
APPLICANT: Edet. John J.
APPLICANT: Rucklineal J. Selet. J. Selet. John J.
APPLICANT: Rucklineal J. Selet. J. Selet. John J. Selet. J. Sel
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Gaps

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Sequence 135, Application US/08127954
Fatent No. 5451512
GENERAL INFORMATION:
APPLICANT: Apple, Raymond J.
APPLICANT: Bugawan, Tecdorica L.
APPLICANT: Erlich, Henry A.
TITLE OF INVENTION: Methods and Reagents for HLA Class I A.
TITLE OF INVENTION: Locus DNA Typing
NUMBER OF SEQUENCES:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.0%; Score 15; DB 1; Length 182; Best Local Similarity 100.0%; Pred. No. 3.9e-07; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                            Query Match 7.0%; Score 15; DB 4; Length 92; Best Local Similarity 100.0%; Pred. No. 2.1e-07; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,954
CURRENT APPLICATION NUMBER: US/09/673,809
CURRENT FILING DATE: 2000-10-20
FRIOR PAPLICATION NUMBER: 98870088.6
FRIOR PLING DATE: 1998-04-20
NUMBER OF SEQ ID NOS: 107
SOTUMBE: PatentIN Ver. 2.1
SEQ ID NO 25
ILENGTH: 92
TYPE: PAT
CRGANISM: Homo sapiens
US-09-673-809-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 0710-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGRAY INDRMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 8873
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (510) 814-2977
TELEPHONE: (510) 814-2977
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 LRRYLENGKETLORA 182
                                                                                                                                                                                                                                                                                                                                                                                                                   146 LRRYLENGKETLORA 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 LRRYLENGKETLORA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-127-954-135
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OTHER INFORMATION: /note= "Rabbit leukocyte antigen (RLA)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.4%; Score 16; DB 3; Length 361; Best Local Similarity 100.0%; Pred. No. 7.2e-08; Matches 16; Conservative 0; Mismatches 0; Indels
                                                                        APPLICANT: Feder, John N.
APPLICANT: Gnirke, Andreas
APPLICANT: Ruddy, David
APPLICANT: Tsuchhhash, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Hereditary Hemochromatosis Gene
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 25, Application US/09673809; Patent No. 6528261; GENERAL INFORMATION: APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: Method for typing of HLA alleles.; FILE REFERENCE: PCT99.86.HLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8907-0088-999
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACIBLE
COMPUTER: IBM PC COMPACIBLE
COMPUTER: Wordberfect Version 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/503,444A
FILING DATE: 14-Feb-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/652,265
FILING DATE: 23-May-1996
APPLICATION NUMBER: 08/632,673
FILING DATE: 16-Apr-1996
APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATTORNEY APPLICATION NUMBER: 08/630,912
FILING DATE: 04-Apr-1996
ATTORNEY ABOUT NUMBER: 28,462
REPERENCE/POCKET NUMBER: 28,462
                                                                                                                                                                                                                                                                        ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
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TELEX: 66141
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
"VPE: amino acid
                           Thomas, Winston J.
Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 EATLRCWALGFYPAEI 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 EATLRCWALGFYPAEI 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Protein
                                                          Drayna,
     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                          USA
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Query Match
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US-08-484-905-105
Sequence 105, Application US/08484905
Sequence 105, Application US/08484905
Sequence 105, Patent No. 5976551
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Complex (MHC) Peterminant and Methods for Using the TITLE OF INVENTION: Determinant and Methods for Using the TITLE OF INVENTION: Determinant
NUMBER OF SEQUENCES: 127
CORRESPONDENCES: 127
ADDRESSEB: Finnegan, Henderson, Farabow, Garrett & ADDRESSEB: Dunner
                                                                     7.0%; Score 15; DB 1; Length 182; 100.0%; Pred. No. 3.9e-07; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                   CITY: Nutley
STATE: New Jersey
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,954
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                                      Sequence 151, Application US/08127954
Patent No. 5451512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
INFORMATION FOR SEQ ID NO: 151:
SEQUENCE CHARACTERISTICS:
LENGTH: 182 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic)
US-08-127-954-151
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 15; Conservative
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RESULT 13
US-08-127-954-151
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COMPUTER: IN IN PC COMPACHASE

OBSTATING SYSTEM, PC-205-NS-DS

ORDERATING SYSTEM, PC-205-NS-DS

ORDERATING SYSTEM, PC-205-NS-DS

ORDERATING SYSTEM: PC-205-NS-DS

ORDERATING SYSTEM: PARTICULUM DAY,

FILING DATE: 07-THE 1934 444,905

FILING DATE: 07-THE 1934

PRICE STATING NAMES: 07-THE 1934

PRICE STATING NAMES: 07-THE 1934

PRICE STATING NAMES: 07-THE 1934

APPLICATION NAMES: 07-THE 1834

PRICE STATING NAMES: 07-THE 1834

APPLICATION NAMES: 07-THE 1834

APPLICANT: MOSTERS: 12-THE 1834

APPLICANT: MOSTERS: 12-THE
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Aag64619 Human can
Aab43986 Human can
Aag64618 Human can
Adf55588 Fragment
Adf55588 Fragment
Abb50296 Human can
Adf55587 Human can
Adf70081 Human hea
Adg26726 Novel hum
Aag00209 Human sec
Abo57084 Human gen
Abb57184 Human gen
Abb5718 Human gen
Abb5718 Human ova
Aam45711 Peptide #Abb5731 Peptide #Abb5731 Peptide #Abb5731 Peptide #Abb5731 Peptide #Abb5731 Peptide #Abb5731 Peptide #Abb34748 Peptide #Abb3
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Human ova
Peptide #
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Peptide #
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                                                                                                                                                                  December 15, 2004, 18:05:00 , Search time 95.8487 Seconds (without alignments) 804.673 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                           1 IAVEYVDDTQFERFDSDAMI.....QRDGEEQTQDTELVETRPAG 215
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Aam67933
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2002273 seqs, 358729299 residues
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                                                                                                                OM protein - protein search, using sw model
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AAB43986
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ADF55588
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ABB34748
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Gapop 60.0 , Gapext 60.0
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1: geneseqp1980s:*
2: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2001s:*
6: geneseqp2003ss:*
7: geneseqp2003bs:*
8: geneseqp2003bs:*
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Maximum DB seq length: 20,0000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
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                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
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Aam81775 Human hae Aam80435 Human hae Aac10522 Human pol Abr58386 Human NoV Abp42373 Human ova Aap80911 Consensus Adf69311 Human lun Aam23760 Human EST Aap70590 Sequence Aap70590 Sequence Aap70590 Sequence Aap70559 Sequence Aap70559 Protein e Adj1259 Protein e					10 ID 6.					,				useful for diagnosing cancer.		coific HLA-F antigen. The 1, and a method for the 1-F antigen. The antigen may be con the protein is used to ds of the patient. The present C HLA-F antigen of the		14; Length 215; te-107; 0; Indels 0; Gaps 0;	DGKDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKET 156
4 AAM81775 4 AAM80435 6 AAM80435 6 AAM80435 5 ABP42373 1 AAB60911 8 AAM23760 1 AAP70155 7 ADP65319 7 ADP65319 8 ADM12521 4 AAM05772 9 AAM06772 5 ADH86497 7 ADB66250 8 ADB663250 8 ADB663250 8 AAM06772 8 AAM06772 9 AAM06772 9 AAM06772 9 AAM06772 9 AAM06772 9 AAM06772	ALIGNMENTS	ein; 215 AA.		ry)	fic HLA-F	ell specific; human.				79566.	79566.			c HLA-F antigen	.2pp; Japanese.	ves to a cancer cell specific : NA encoding the antigen, and cancer cell specific HLA-F ant diagnose cancer, in which the tribodies in bodily fluids of the cancer cell-specific HLA		5.3%; Score 119; DB 00.0%; Pred. No. 3.4« ve 0; Mismatches	WTAADTVAQITQRFYBAEBY
33.22 33		1 9 364619 standařd; protein;	364619;	-SEP-2001 (first ent	Human cancer cell speci	A-F antigen, cancer c	omo sapiens.	2001095584-A.	-APR-2001.	-SEP-1999; 99JP-002	-SEP-1999; 99JP-002	(EEGAW/) EGAWA K. (MEDI-) MEDINET KK. (KIMU/) KIMURA K.	I; 2001-360493/38. PSDB; AAH45557.	vel cancer cell-specifi	aim 1; Page 11-12; 1	invention relates nation includes DNA ration of the cand in a method to did anti-HIA-F antilisnce represents the attion	equence 215 AA;	Match local Similarity 1 es 119; Conservati	97 DGKDYISLNEDLRS
00000000000000000000000000000000000000		RESULT 1 AAG64619 ID AAG6	AA AC AAG	12	•	KW HLA	I	чP	10	30	30		DR WPI	XX PT Nove	ប	XX CC This CC inves CC prepi	Ω	Query Best Lo Matche	δò

AAB43986

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cancer. The agent comprises a portion or a complete sequence of a human leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of presenting a cancer-cell specific antigen transformed with HLA-F DNA, or yetcoxic T lymphocyte (CTL) inducer which induces CTL which is non-specific to an organ, is unrestricted to the major histocompatibility complex (MHC) and specific to a cancer cell, and an anti-HLA-F antibody. The agent of the invention is useful for treating or preventing cancer. A cell capable of presenting or acancer-cell specific antigen is useful for measuring HLA-F antigen and cancer-cell specific antigen. Sequence represents part of the human cancer-cell specific HLA-F antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97 DGKDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKET 156
97 DGKDYISLNEDLRSWTAADTVAQITQRFYEAEBYABEFRTYLBGECLBLLRRYLENGKET 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 DGKDYISLNEDLRSWTAADTVAQITQRFYBABEFRTYLBGBCLBLLRRYLBNGKBT 156
                                                                                                                  157 LQRADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAG 215
                                                                                                                                                         157 LORADPPKAHVAHHPISDHEATLRCWALGFYPABITLTWQRDGEEQTQDTELVETRPAG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157 LQRADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agent for preventing and treating cancer, comprising human leukocyte antigen-F DNA, or a plasmid or viral vector comprising the DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to an agent for preventing or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte, CTL; major histocompatibility complex; MHC; cancer cell; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fragment #2 of human cancer-cell specific HLA-F antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cancer; human leukocyte antigen-F; HLA-F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; SEQ ID NO 6; 19pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                           ADF55589 standard; protein; 215 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAR-2002; 2002JP-00088991.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-FEB-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-486263/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ADF55586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADF55589;
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                                                                                                                                                                                                                                                                                                                                       ADF55589
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RESULT 3

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AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB4239. The proteins can have activities based on the tissues and calls the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antitheumatic; antidiathriticismandory; antithyroid; antidiamentary; immunomodulator; antidiamentary; insurportective; cardiant; thrombolytic; coagulant; contropic; vasotropic; antipsoriatic and antianglogenic. The polymucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polymucleotides, polypeptides, antibodies, agonists and antagonists from the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune cells, to treat disorders of haematopoietic cells, autoimmune rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and charmation, cancers, cardiovascular disorders, neurological disease and approaches and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 DGKDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKET 156
                                                                                                                                                                                      diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidabetic; antiasthmatic; antirhemmatic; antidabetic; antivarial; antifulamentor; antiturorial; antiturinflammatory; antiturorial; antiturory; thrombolytic; coaquiant; noctropic; vasotropic; antipscriatic; antiantic; coaquiant; noctropic; vasotropic; antipscriatic; antianglogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; neurological disease; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer.
                                                                                                                                                                      Human; cancer associated gene; cancer antigen; detection; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.3%; Score 119; DB 3; Length 271
100.0%; Pred. No. 4.1e-107;
tive 0; Mismatches 0; Indels
                                                                                                                            Human cancer associated protein sequence SEQ ID NO:1431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 2115-2116; 2352pp; English.
AAB43986 standard; protein; 271 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAR-2000; 2000WO-US005882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAR-1999; 99US-0124270P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.0
Matches 119; Conservative
                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-587533/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAC78195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 271 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200055350-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-SEP-2000.
                                                                                   08-FEB-2001
                                           AAB43986;
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WPI; 2003-486263/46.
N-PSDB; ADF55585.
                                                                                                                                                                            EGAWA K.
MEDINET KK.
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                                                                                                                                                                                                        (KIMU/) KIMURA Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 274 AA;
                                                                 JP2003012544-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP2001095584-A.
                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo gapiens
                                                                                            15-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG64617;
                                                                                                                                                                             (EGAW/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to a cancer cell specific HLA-F antigen. The invention includes DNA encoding the antigen, and a method for the preparation of the cancer cell specific HLA-F antigen. The antigen may be used in a method to diagnose cancer, in which the protein is used to detect anti-HLA-F antibodies in bodily fluids of the patient. The present sequence represents the cancer cell-specific HLA-F antigen of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 DGKDYISLNEDLRSWTAADTVAQITQRFYEAEEYABEFRTYLEGGECLELLRRYLENGKET 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 DGKDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKET 178
                            157 LORADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWORDGEEOTODTELVETRPAG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 LORADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.3%; Score 119; DB 4; Length 274; 100.0%; Pred. No. 4.1e-107; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fragment #1 of human cancer-cell specific HLA-F antigen.
                                                                                                                                                                                         Human cancer cell specific HLA-F antigen SEQ ID 5.
                                                                                                                                                                                                                    HLA-F antigen; cancer cell specific; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cancer; human leukocyte antigen-F; HLA-F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 10-11; 12pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADF55588 standard; protein; 274 AA.
                                                                                                       AAG64618 standard; protein; 274 AA.
                                                                                                                                                                                                                                                                                                                                99JP-00279566.
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                                                                                                                                                              (first entry)
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es 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-360493/38.
                                                                                                                                                                                                                                                                                                                                                                                    EGAW/) EGAWA K.
MEDI-) MEDINET KK.
                                                                                                                                                                                                                                                                                                                                                                                                               KIMU/) KIMURA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAH45556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 274 AA;
                                                                                                                                                                                                                                                                          JP2001095584-A.
                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                30-SEP-1999;
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                                                                                                                                                              12-SEP-2001
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The present invention relates to an agent for preventing or treating cancer. The agent comprises a portion or a complete sequence of a human leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of presenting a cancer-cell specific antigen transformed with HLA-F DNA, or a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte (CTL) inducer which induces CTL which is non-specific to an organ, is unrestricted to the major histocompatibility complex (MHC) and specific to a cancer cell, and an anti-HLA-F antibody. The agent of the invention is useful for treating or preventing cancer. A cell capable of presenting a cancer-cell specific antigen is useful for measuring HLA-F antigen and for diagnosing cancer. The present sequence represents part of the human cancer-cell specific HLA-F antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 DGKDYISLNEDLRSWTAADTVAQITQRFYBAEEYAEEFRTYLEGECLELLRRYLENGKET 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 DGKDYISINEDIRSWTAADTVAQITQRFYEABEFYABEFFTYLEGECLELIRRYLENGKET 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 LORADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGBEQTQDTELVETRPAG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agent for preventing and treating cancer, comprising human leukocyte antigen-F DNA, or a plasmid or viral vector comprising the DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.3%; Score 119; DB 7; Length 274; 100.0%; Pred. No. 4.1e-107;
cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte major histocompatibility complex; MHC; cancer cell; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; SEQ ID NO 5; 19pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG64617 standard; protein; 362 AA.
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                                                                                                                                                                                                                                                                                                                                                                                  27-MAR-2002; 2002JP-00088991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-MAR-2001; 2001JP-00090121
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                                                                                                                                                                                                                          This invention relates to a cancer cell specific HLA-F antigen. The invention includes DNA encoding the antigen, and a method for the preparation of the cancer cell specific HLA-F antigen. The antigen may be used in a method to diagnose cancer, in which the protein is used to detect anti-HLA-F antibodies in bodily fluids of the patient. The present sequence represents the cancer cell-specific HLA-F antigen of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 DGKDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKET 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGKDYISLNEDLRSWTAADTVAQITQRFYEAEBYAEBFRTYLEGECLELLRRYLENGKET 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 LQRADPPXAHVAHHPISDHBATLRCWALGFYPABITLTWQRDGBEQTQDTBLVETRPAG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 LORADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGESOTODTELVETRPAG 258
                                                                                                                                                      Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 119; DB 4; Length 36
Pred. No. 5.1e-107;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA-Cw ovarian tumour marker protein, SEQ ID NO:82.
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                                                                                                                                                                                                                                                                                                                                                                                   55.3%; Scor. No. ... 100.0%; Pred. No. ... 0; Mismatches ...
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                                                                                                                                                                                          Disclosure; Page 9-10; 12pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB50296 standard; protein; 362 AA
99JP-00279566.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 119; Conservative
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                                                                                                       WPI; 2001-360493/38.
                                (EGAW/) EGAWA K. (MEDI-) MEDINET KK.
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                 (KIMU/) KIMURA K.
                                                                                                                    N-PSDB; AAH45555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABA83122
                                                                                                                                                                                                                                                                                                                                                                  Sequence 362 AA;
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 30-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                    invention
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The invention relates to methods for diagnosing and prognosing ovarian tumours in an individual via the detection and measurement of the expression of ovarian tumour marker genes (ABA83081-ABA83169, ABA83180, ABA83181 and ABA83189). The methods of the invention are useful for detecting an ovarian tumour in a patient, for identifying an individual at increased risk for developing ovarian cancer, in prognostic tests for assessing the relative severity of ovarian cancer, in tests for monitoring abatient in remission from ovarian cancer, in tests for monitoring disease status in a patient being treated for ovarian cancer. The methods can additionally be used to identify a particular tumour as being an ovariant undour (i.e., an epithenial ovarian tumour selected from serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma, concernioms, andometrioid carcinoma, undifferentiated carcinoma, clear cell adenocarcinoma, endometricid carcinoma, undifferentiated carcinoma, clear cell adenocarcinoma, concernioma, adenocibroma and Brenner tumour The ovarian tumour marker genes of the invention were identified oversors serial analysis of gene expression) and were found to be coverexpressed in a broad variety of ovarian epithelial tumour cells crelative to normal ovarian epithelial cells. The marker genes are membrane proliferation and in protein folding, and many of these are membrane proliferation and in protein folding, and many of these are membrane construction and in protein folding, and menter of adaptosic and an ordinal analysis of the regulation of cell consider the constant of their use as diagnostic and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 DGKDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEFFRTYLEGECLELLRRYLENGKET 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200 LQRADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 LQRADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAG 215
                  Detecting and identifying ovarian tumor, identifying increased risk for developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prognostic markers, the ovarian tumour marker genes or their encoded proteins may be used as therapeutic targets for the treatment and prevention of ovarian cancer. Sequences ABBS0257-ABBS0299 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cancer; human leukocyte antigen-F; HLA-F; cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; cancer cell; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins encoded by ovarian tumour marker genes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.3%; Score 119; DB 4; Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 5.1e-107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human cancer-cell specific HLA-F antigen.
                                                                                                                                                Claim 23; Page 126-127; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADF55587 standard; protein; 362 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence 362 AA;
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The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of amarker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (SI) whose expression levels increase when respiratory epithelial calls are stimulated with interleukin-13; or (b) a group of genes (SI) whose expression levels increase when respiratory epithelial calls are stimulated with interleukin-13. Also described: (1) a reagent (1) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (5) a namimal model for bronchial asthma or chronic obstructive pulmonary disease; (6) a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, (6) a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, (7) a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene or an antisense nucleic acid corresponding to a portion of the marker gene or an antisense nucleic acid corresponding to a portion of the marker gene a chronic obstructive pulmonary disease, on which a procein encoded by a marker gene; and (7) a DNA chip for testing for c spreading for a chronic obstructive pulmonary disease, on which a procein an antisethmatic activities, and can be used in gene therapy. The method is useful for testing for or screening for a therapeutic aspent for bronchial asthma or chronic obstructive pulmonary disease. The procein an antisethmatic activities, and can be used in gene therapy. The method is sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 DGKDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKET 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 DGKDYISLNEDLRSWTAADTVAQITQRFYEAEBYAEBFRTYLEGECLELLRRYLENGKET 199
  Testing for bronchial asthma or chronic obstructive pulmonary disease by comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a healthy subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 LORADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQRADPPKAHYAHHPISDHEATLRCWALGFYPAEITLTWQRDGBEQTQDTELVETRPAG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transplant rejection; immune system; rheumatoid arthritis; lupus; inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.3%; Score 119; DB 8; Length 36; clarity 100.0%; Pred. No. 5.1e-107; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein encoded by mRNA of the invention #110.
                                                                                                                Example 11; SEQ ID NO 624; 241pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADP12500 standard; protein; 362 AA
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Matches 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to an agent for preventing or treating cancer. The agent comprises a portion or a complete sequence of a human leukocyte antigen (HLA)-F DNA. Also disclosed is a cell capable of presenting a cancer-cell specific antigen transformed with HLA-F DNA, or a plasmid or viral vector comprising HLA-F DNA, a cytotoxic T lymphocyte (CTL) inducer which is non-specific to an organ, is unrestricted to the major histocompatibility complex (MHC) and specific to a cancer cell, and an anti-HLA-F antibody. The agent of the invention is useful for treating or preventing cancer. A cell capable of presenting a cancer-cell specific antigen is useful for measuring HLA-F antigen and for diagnosing cancer. The present sequence represents human cancer-cell specific antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 DGKDYISLNEDLRSWTAADTVAQITQRFYEAEEFYAEEFRTYLEGECLELLRRYLENGKET 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 DGKDYISINEDIRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKET 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 LQRADPPKAHVAHHPISDHEATLRCWALGFYPABITLIWQRDGBEQTQDTELVETRPAG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 LQRADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bronchial asthma; chronic obstructive pulmonary disease; respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
                                                                                                                                                                                                  Agent for preventing and treating cancer, comprising human leukocyte antigen-F DNA, or a plasmid or viral vector comprising the DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.3%; Score 119; DB 7; Length 362; 100.0%; Pred. No. 5.1e-107; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marker gene related amino acid sequence SEQ ID NO:624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H,
                                                                                                                                                                                                                                                                Claim 5; SEQ ID NO 4; 19pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADJ75372 standard; protein; 362 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-AUG-2003; 2003EP-00254857.
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20-MAR-2003; 2003JP-00077212.
27-MAR-2001; 2001JP-00090121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-MAY-2004 (first entry)
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1es 119; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy; marker.
                                                                                                                                 WPI; 2003-486263/46,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-193155/19.
                                        EGAW/) EGAWA K.
MEDI-) MEDINET KK.
                                                                                    (KIMU/) KIMURA Y.
                                                                                                                                                         N-PSDB; ADF55584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 362 AA;
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The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet. lung, bone marrow or stem cell transplant rejection, in an exentiansplant rejection or mechanical organ replacement rejection, in an individual. The method is also useful in diagnosing the immune status of diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple selerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a protein that is encoded by the mRNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGKDYISLNEDLRSWTAADTVAQITQRFYBABEYAEBFRTYLEGECLELLRRYLENGKET 156
                                                                                                                                                                                                       Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 DGKDYISLNEDLRSWITAADIVAQITQRFYEAEBYAEBFRIYLBGBCLBLLRRYLBNGKBT 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 LORADPPKAHVAHHPISDHEATLRCWALGFYPABITLIWQRDGEBQTQDTELVETRPAG 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Huntington's disease; osteoarthritis; LHON; Leber's hereditary optic neuropathy; LHON; mitochondrial encephalopathy lactic acidosis and stroke; MELAS; myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer; neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic; osteopathic; optichalmological; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human heat mitochondrial protein as a therapeutic target SeqID1887.
                                                                                                    Fry K, Woodward R, Ly N, Prentice J, Morris M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 55.3%; Score 119; DB 8; Length 36. Local Similarity 100.0%; Pred. No. 5.1e-107; Local 119; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mitochondrial; human; screening assay; diabetes mellitus;
                                                                                                                                                                                                                                                                                                          Claim 65; SEQ ID NO 2509; 1762pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ70081 standard; protein; 442 AA.
                                                            (EXPR-) EXPRESSION DIAGNOSTICS INC
24-APR-2002; 2002US-00131831.
20-DEC-2002; 2002US-00325899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-APR-2003; 2003WO-US010870.
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                                                                                                                                                                 WPI; 2004-400724/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 362 AA;
                                                                                                    Wohlgemuth J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                           Rosenberg S;
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                                                                                                                                                                                                                                                                      the genes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97
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This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with altered mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's heredicary optic neuropathy (LHON), mitochondrial concephalopathy lactic acidosis and stroke (MELAS), mycolonic epilepsy ragged red fibre syndrome (MERRP) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, antidiabetic, anticohondrial protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 DGKDYISLNEDLRSWTAADTVAQITQRFYEAEEFAREFRTYLEGECLELLRRYLENGKET 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 DGKDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKET 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200 LQRADPPKAHVAHHDISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 LORADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGBEQTQDTELVETRPAG 215
                                                                                                                                                                                                      Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                Glenn GM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 442;
                                                                                                                Gibson BW, Taylor SW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.3%; Score 119; DB 7; Le
100.0%; Pred. No. 6.1e-107;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1887; 180pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG26726 standard; protein; 677 AA.
                                                                                                                Zhang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAR-2000; 2000US-00540217.
17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-FEB-2002 (first entry)
                                                                            BUCK-) BUCK INST AGE RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 119; Conservative
                                                                                                                  Fahy ED,
                                                                                                                                                                      WPI; 2003-845369/78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                   with the disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 442 AA;
                                                          (MITO-) MITOKOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200175067-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-2001.
                                                                                                                                  Warnock DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG26726;
                                                                                                                Ghosh SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, ollgomers, and for chomosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed sequence tags for identifying expressed carivity of (II) as useful in gene therapy techniques to restore normal carivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention Note: The sequence data for this partent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 DGKDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKET 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          449 DGKDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKET 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 LORADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTODTELVETRPAG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           509 LQRADPPKAHVAHHPISDHEATLRCWALGFYPAEITLITWQRDGEBQTQDTELVETRPAG 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 55.3%; Score 119; DB 4; Length 677; Local Similarity 100.0%; Pred. No. 8.6e-107; les 119; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                 Claim 20; SEQ ID NO 57085; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein, SEQ ID NO: 4290.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG00209 standard; protein; 120 AA.
                                             Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-FEB-2000; 2000EP-00200610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-OCT-2000 (first entry)
                                             Drmanac RT, Liu C,
                                                                                     WPI; 2001-639362/73.
N-PSDB; AAS90913.
(HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 677 AA;
                                                                                                                                                                                                                      biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP1033401-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36-SEP-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 IAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYWEWTTGYAKANAQTDRVALRNLL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 IAVEYVDDIQFLRFDSDAAIPRMEPREPWVEQEGPQYWEWTTGYAKANAQTDRVALRNLL 60
                                                                                                                                                                                                                                                 New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; SEQ ID NO 4290; 71pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 35.8%; Score 77; DB 3; Length 120 Local Similarity 100.0%; Pred. No. 1.4e-66; es 77; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                                                     Dumas Milne Edwards J, Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human genome derived single exon protein #3318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABOS7084 standard; protein; 96 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 RRYNQSEAGSHTLOGMN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Penn SG, Rank DR, Hanzel DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 RRYNOSEAGSHTLOGMN 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-APR-2002; 2002US-00029386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-APR-2002; 2002US-00029386.
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                                                                                                                                               WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-119264/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                               N-PSDB; AAC00215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence 120 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2003194704-A1.
(GEST ) GENSET.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 adino acids of any of the 6888 amino acid sequences ("Illy defined in the specification. The probe is a single exon probe that wherefalses under high stringency conditions to a nucleic acid molecule expression (comprising a plurality of single exon nucleic acid molecule expression (comprising a plurality of single exon nucleic acid molecule expression (comprising a plurality of single exon nucleic acid molecule expression (comprising a plurality of single exon nucleic acid and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a vector comprising the single exon and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a vector comprising at least 8 contiguous amino acids of any of the above- mentioned amino acid such any of the above- mentioned any of solated antibody that binds specifically to a peptide cited above, a customer desiring to measure desiring and car by subscription, and a computer-readable expression analysis. The probes may be used as tools for surveying human gene expression analysis. The probes may be used as tools for surveying croaded above, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying croaded above, methods and apparatus are useful in detections in the probes are used in identifying and characterising general expression in expressing the probes are used in identified and contain or the probes or in New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for Claim 45; SEQ ID NO 30718; 80pp; English. surveying tissues.

Sequence 96 AA;

segdata.uspto.gov/sequence.html?DocID=20030194704

0; Gaps Score 55; DB 8; Length 96; Pred. No. 2.8e-45; 0; Mismatches 0; Indels 25.6%; Scor. 100.0%; Pred. No. 0; Mismatches 55; Conservative Query Match Best Local Similarity Matches

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Human ovarian antigen HPDRT37, SEQ ID NO:4063. ABP42931 standard; protein; 186 AA. 22-AUG-2002 (first entry) ABP42931; RESULT 15 ABP4293

Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovaliation; polytycstic ovary syndrome; pCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; duug screening; gene therapy; chromosome mapping; forensic analysis;

antibody preparation, cytostatic; immunomodulatory, neuroprotective; antiinflammatory; gynaecological; reproductive.

Homo sapiens.

WO200200677-A1.

03-JAN-2002.

07-JUN-2001; 2001WO-US018569.

07-JUN-2000; 2000US-0209467P.

(HUMA-) HUMAN GENOME SCI INC.

Birse CE, Rosen CA;

WPI; 2002-147878/19. N-PSDB; ABQ56008 Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological

Claim 11; SEQ ID NO 4063; 2922pp; English.

diseases.

The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABO5411-ABO56315), and also encompasses polypeptides 90% identical and polymolecutdes 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigens of covarian antigens, and the use of ovarian antigens, and the use of ovarian antigens, and the use of ovarian antigens polymolecutdes and breast cancer, and the atstatic tumours of ovarian or breast origin, reproductive system covary syndrome, ovarian or sets, and toxic polycystic ovary syndrome, ovarian or sets, and ovarian concer and dysmenorrhoea), endocrine disorders (e.g., chlamylydia, HIV, toxoplasmostis, and toxic vaginitis), immune disorders (e.g., mastifis, ophoritis and vaginitis), immune disorders (e.g., anaemia), cardiovascular disorders (e.g., anaemia), cardiovascular disorders and urinary system disorders. Ovarian antigen polypetides and urinary system disorders. Ovarian antigen of compounds which modulate ovarian antigen of inforensic analysis, and the present system of sequence represents a human ovarian antigen of the proprise or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence data for this patent did not form part of the present sequence data for this patent did not form part of the present sequence data for this patent did not form part of the present sequence as human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the present sequences.

Sequence 186 AA;

0; Gaps Length 186; 0; Indels 24.2%; Score 52; DB 5; L. 100.0%; Pred. No. 3.9e-42; tive 0; Mismatches 0; 1 Similarity 100.0 52; Conservative Query Match Best Local S Local Matches

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1 GSHSLRYFSTAVSRPGRGEP......QRYTCHVQHEGLPQPLILRW 274
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1825181 Total number of hits satisfying chosen parameters: 1825181 segs, 575374646 residues 0 Word size : Searched:

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Scoring table:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries UniProt_02:*
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2: uniprot_trembl:* Database :

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STIMMARTES

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Cad89636 macaca mu		CAD89636	N	351	18.2	20	42
Q70pm0 macaca mula		Q70PM0	N	351	18.2	20	4.4
		Q61796 Q70PL7	N (1	365 351	18.3	50	4 4 0 5
Bad18842 actus tri		BAD18842	7	355	19.3	23	38
Q767w6 aotus trivi		Q767W6	7	355	19.3	53	3.7
Cad83079 macaca mu		CAD83079	0	354	19.3	53	36
Q70sh4 macaca mula		Q70SH4	7	354	19.3	53	35
Q6i7a9 macaca fasc		Q617A9	N	365	20.1	52	34
Q6i7a3 macaca fasc		Q617A3	N	365	21.2	28	33
S SOSSSEE - CONSTRU		CAD83073	~	354	21.2	28	32

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 EWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 EWITGYAKANAQIDRVALRNILRRXNQSEAGSHILQGMNGCDMGPDGRLLRGYHQHAYDG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 KDYISLNEDLRSWTAADTVAQITQRFYBABEYABBFRTYLBGECLBLLRRYLBNGKETLQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 KDYISLNEDLRSWTAAADTVAQITQRFYBABEYAEEFRTYLEGECLELLRRYLENGKETLQ 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT 240
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                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                           Liu Y., Xu L., Zeng Y., He X.,

Liu Y., Xu L., Zeng Y., He X.,

Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

R Goldsolo (JAN-2003) to the EMBL/GenBank/DDBJ databases.

R GO; GO:0016020; C.membrane; IEA.

GO; GO:0006955; P:immune response; IEA.

R InterPro; IPR00110; Ig-like.

R InterPro; IPR001306; Ig-MHC.

R InterPro; IPR001306; Ig-MHC.

R Pfam; PF07654; Cl. = et.; I.

P Ffam; PF07654; Cl. = et.; I.

P R PR015; RR01638; MHC. I; I.

P R ProDom; PD000050; MHC. I; I.

P R POSITE; PS00290; IG-IKE; I.

R PROSITE; PS00290; IG-IKE; I.
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324 AA; 36518 MW; E3E028177D2716F4 CRC64;
                  01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
MMC class I antigen (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 274; Conservative
                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                    Name=HLA-F;
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MHC class Ib antigen (HLA-F protein).
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                    Name=HLA-F;
Homo sapiens (Human).
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TISSUE=Lymph;
                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                  PubMed=14705989;
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EMBL;
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EMBL;
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EMBL;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 324;
                                                                                                                                                                                                                                                                                                                                                                               He X., Xu L., Liu Y., Zeng Y.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
Bubmitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
Bubmit, A2916682; AA037689.1; -.
BASP; A29366, LikeA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
InterPro; IPR0031010; Ig-like.
InterPro; IPR003107; Ig_cl.
InterPro; IPR00306; Ig MHC.
InterPro; IPR00309; MHC.
InterPro; IPR00109; MHC.
InterPro; IPR01009; MHC.
InterPro; IPR01009; MHC.
InterPro; IPR01010; Ig-like.
Pfam; PF00129; MHC_I:
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Last sequence update)
Last annotation update)
                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last Sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Nonclassical MHc class I antigen (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 274; DB 2; L
100.0%; Pred. No. 3.3e-280;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 FOKWAAVVVPSGEEORYTCHVQHEGLPOPLILRW 274
  241 FOKWAAVVVPSGEEORYTCHVQHEGLPOPLILRW 274
                      258 FOKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 FOKWAAVVVPSGEEQRYTCHVQHEGLPQPLILKW 291
                                                                                                                                    PRT; 324 AA.
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ProDom, PD000050, MHC.1; 1.
SMART, SM00407, IGC1, 1.
PROSITE; PS0835; IG LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.0
Matches 274; Conservative
                                                                                                                                    PRELIMINARY;
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01-MAR-2002 (
01-MAR-2002 (
01-OCT-2004 (
                                                                                                                                                                                                                                                  Name=HLA-F;
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Q861F0;
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                                                                                             RESULT 2
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RC TISSUE-Lymph.

RX MIDINE-2238252;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Strausberg R.L., Feingold E.A., Grouse L.H., Schaefer C.F., Bhat N.K.,

RA Strausberg R.L., Seeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,

RA Alachula S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hsieh F.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., Worley K.C., Hale S., Garcia A.M. Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia A.M. Gay L.J., Hulyk S.W.,

RA Richards S., Worley K.C., Hale S., Garcia R.D., Dickson M.C.,

RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Richards S.A., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Noriski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.,

R. "Generation and initial analysis of more than 15,000 full-length human
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBL_TaxID=9606,
                                                                                                                                                                                              SEGUENCE FROM N.A. Islliams L.M., Moore Y., Geraghty D.E., Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      He X., Xu L., Liu Y., Zeng Y.; "Identification of a novel HLA-F allele - HLA-F*010102."; Tissue Antigens 63:181-183(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. He X., Zeng Y.; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AF523285; AAM74980.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases
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Proc. Natl. Acad: Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 KDYISLNEDLRSWTAADTVAQITQRFYEAEBFYAEBFRTYLEGECLELLRRYLENGKETLQ 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 EWTTGYAKANAQIDRVALRNILRRYNQSBAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 346;
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100.0%; Score 274; DB 2; Length 346;
Best Local Similarity 100.0%; Pred. No. 3.5e-280;
Matches 274; Conservative 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Submitred (JUN-2204) to the EMBL/GenBank/DDBJ databases.
EMBL; AY645747, AAT7230.1;
SEQUENCE 346 AA, 39079 WW; 8C370BFB40B1581B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  346 AA; 39051 MW; D4782AA4697D57B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch
100.0%; Score 274; DB 2; L
al Similarity 100.0%; Pred. No. 3.5e-280;
274; Conservative 0; Mismatches 0;
                                                                                                                                                                                                 GG; GG: GG: GG: Tringeral to membrane; IEA. GG; GG: GG: GG: FG: Tringeral to membrane; IEA. GG; GG: GG: GG: FG: Tringeral to membrane; IEA. InterPro; IPR007110; IG-1ike.
InterPro; IPR003597; IG-1ike.
InterPro; IPR00306; IG-MC.
InterPro; IPR00306; IG-MC.
InterPro; IPR00306; IG-MC.
InterPro; IPR003089; MFC.
Pfam; PF07654; CI-eet; I.
Pfam; PF07654; MFC. I.
ProDom; PR000069; MFC. I.
PR0DOM; PR000069; MFC. I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 FOKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 FQKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
EMBL; AY645751; AAT73234.1; EMBL; AY645752; AAT73235.1; EMBL; AY645756; AAT73239.1; EMBL; AY645756; AAT73239.1; EMBL; AY645757; AAT73240.1; EMBL; AY645759; AAT73241.1; EMBL; AY645759; AAT73241.1; EMBL; AY645759; AAT73241.1; EMBL; AY645759; AAT73242.1; AY645759; AAT73242.1; AY645759; AAT73242.1; AY645759; AAT73242.1; AY645759; AY64759; AY64759; AY645759; AY64759; AY64759; AY64759; AY64759; AY64759; AY64759; AY64
                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM0407; IGC1; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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RECORDINGE-22388257; PubMed=12477932;

RECORDINGE-22388257; PubMed=12477932;

Record R.D., Colling F.S., Wagner L., Shamen C.M., Schuler G.D.,

R. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

R. Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

R. Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B. Distochero M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

R. Stapleton M. J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

R. And S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R. Bosak S.A., McEvan P.J., McKernan K.J., Male M.N., Gay L.J., Hulty S.W.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulty S.W.,

R. Halton D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

R. Halton B., Ketteman M., Madan A., Rodriques S., Sanchez A.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Raywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

R. Jones S.J., Marra M.A.;

R. Generation and initial analysis of more than 15,000 full-length human

RT and mouse CDNA sequences.",

P. Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAGDGT 240
                                                                                                                                                               EWITGYAKANAQIDRVALRNLLRRYNQSEAGSHILQGMNGCDMGPDGRLLRGYHQHAYDG 120
                                                                                                                                                                                                                                       82 EWITGYAKANAQIDRVALRNLLRRYNQSEAGSHILQGMNGCDMGPDGRLLRGYHQHAYDG 141
                                                                                                                                                                                                                                                                                                                               121 KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEBFRIYLEGECLELLRRYLENGKETLØ 180
                                                                                                                                                                                                                                                                                                                                                                                                       142 KDYISLNEDLRSWIAADIVAQIIQRFYBAEBYABBFRIYLBGBCLBLLRRYLENGKBILQ 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 RADPPKAHVAHHPISDHBATLRCWALGFYPABITLTWQRDGBBQTQDTBLVBTRPAGDGT 261
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GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 60
                                                                       22 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 81
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
EMBL: BC062991; AAH62891.1; -
SEQUENCE 346 AA; 39051 MW; D4782AA4697DS7B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 274; DB 2; L ilarity 100.0%; Pred. No. 3.5e-280; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 FOKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 FQKWAAVVVPSGEEQRYTCHVQHEGLPQPLILEW 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 346 AA
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RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT 240
                       EWITGYAKANAQIDRVALRNILRRYNQSEAGSHILQGMNGCDMGPDGRLLRGYHQHAYDG 120
                                                   EWITGYAKANAQIDRVALRNILRRYNQSEAGSHTLQGMNGCDMGFDGRLLRGYHQHAYDG 141
                                                                                                                                                               142 KDYISLNEDLRSWTAADTVAQITQRFYEAEBYAEBFRTYLEGECLELLRRYLENGKETLQ 201
                                                                                                                                                                                                                                                           261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P30511; OPTP68;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
HLA class I histocompatibility antigen, alpha chain F precursor (HLA F antigen) (Leukocyte antigen F) (CDA12).
Name=HLA-F; Synonyms=HLA-F, HLA-5.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [3]
SEQUENCE FROM N.A.
MEDLINE=20189517; PubMed=10727083;
MEDLINE=20189517; PubMed=10727083;
MEDLINE=20189517; PubMed=10727083;
MOLTIER B., Coriton O., Andrieux N., Carn G., Lepourcelet M.,
Mottier S., Dreano S., Gatius M.T., Hitte C., Soriano N., Galibert F.;
"A 356-Kb sequence of the subtelomeric part of the MHC class I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=9011605; PubMed=1688605;
Geraghty D.E., Wei X., Orr H.T., Koller B.H.;
Geraghty D.E., wai X., Orr H.T., Koller B.H.;
"Human leukocyte antigen F (HLA-P). An expressed HLA gene composed of a class I coding sequence linked to a novel transcribed repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-2235763; PubMed-14574404; DCI-10.1038/nature02055; MEDLINE-2235763; PubMed-14574404; DCI-10.1038/nature02055; Mungal A.J., Palmer S.A., Sims S.K., Edwards C.A., Ashurst J.L., Wilming L. Jones M.C., Horton R., Hunt S.E., Scott C.E., Glibert J.G.R., Clamp M.E., Bathel G., Minne S., Ainscough R., Almeida J.P., Ambrose K.D., Andrews T.D., Ashwell R.I.S. Babbage A.K., Bagguley C.L., Bailey J., Banerjee R., Barker D.J., Barlow K.F., Bates K., Reare D.M., Beasley H., Beasley O., Bird C.P., Blakey S.E., Bray-Allen S., Brook J., Brown A.J., Brown J.Y., Chapman J.C., Clark S.Y., Clee C.M., Cleeg S., Cobley V., Collins J.E., Collan L.K., Corby N.R., Coville G.J., Culley K.M., Dhami P., Davies J., Dunn M., Earthrowl M.E.,
                                                                                                                   KDYISLNEDLRSWTAADTVAQITQRFYBAEBYAEBFRTYLEGGECLELLRRYLENGKETLQ
                                                                                                                                                                                                                                                           RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shiina S., Taniya G., Oka A., Inoko H.; H.; Shiina S., Taniya G., Oka A., Inoko H.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [2] SEQUENCE FROM N.A. SEDUENCE FROM N.A. SEDUENCE FROM N.A. LUTY D., EDSTEEN H., Holmes N.; "The human class I MHC gene HLA-F is expressed in lymphocytes."; Int. Immunol. 2:531-537(1990).
                                                                                                                                                                                                                                                                                                         FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
                                                                                                                                                                                                                                                                                                                                                     262 FOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 362 AA
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Elington A.E., Evans K.A., Faulkner L., Francis M.D., Frankish A., allington A.E., Evans K.A., Faulkner L., Garnett J., Ghori M.J., alliby L.M., Gillson C.J., Glithero R.J., Grafham D.V., Grant M., alribble S., Griffiths C.J., Glithero M.N.D., Halls K.S., Hambon S., Harley J.L., Hart E.A., Heath P.D., Heathcott R., Andres S.J., Humphray S.J., Humphray S.J., Humphray S.J., Humphray S.J., Kimberley A.M., King A., Loird G.K., Langford C., Laviors M.D., Loveland J.B., Loveland J.B., Mcrant D.A., Leversha M., Lloyd C.R., Lloyd D.M., Andres G.B., Loveland J.B., Mcrant D.T., Mcraren S.J., McLay K., Lovel J.M., Marlen G.L., McLaren S.J., McLay K., McMurray A., Moore M.J.F., Mullikin J.C., Niblett D., Nickerson T., Mcwik K.L., Oliver K., Owerton-Larty E.K., Parker A., Pack R.J., Phillimore B.J.C.T., Phillips S. Plumb R.W., Perk M., Ramby S.A., Sicce C.M., Ross M.T., Searle S.M., Schre S.L., Stwice C.D., Smith M., Spraggon L., Squares S.L., Stward C.A., Sycamore N., Tamlyn-Hall G., Tester J., Milley D.J., Willer T.E., Wood J.M., Wray P.W., Whytt J.C., Young L., Younger R.M., Bentley D.R., Tromas A., Tromas A., Thoby B., Whiteker H., Willed A., Willey D.J., Wilmer T.E., Wood J.M., Wray P.W., Whyth D.Ms sequence and analysis of human chromosome 6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 425:805-811(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune system.
-- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-
microglobulin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIA class I histocompatibility antigen, alpha chain F. Extracellular alpha-1. Extracellular alpha-2. Extracellular alpha-3. Connecting peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNATT, SW00407, IGC1, I.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS0290; IG MHC; 1.
Glycoprotein; MHC I; Polymorphism; Signal; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               By similarity.
By similarity.
N-linked (GlCNAc. . .) (By
S -> P (in dbSNP:1736924).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytoplasmic tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AP055066, AAC24827.1; -.
EMBL, AP000521; BAB63337.1; -.
EMBL, AL022723; CAB46623.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X17093; CAA34947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
DISULFID
CARBOHYD
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
DOMAIN
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/FTId=VAR 018327

262 FOKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 295

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MEDINE=2238257, PubMed=12477932;

RECONSIDERE-2238257, PubMed=12477932;

REDINE=2238257, PubMed=12477932;

REDINE=2238257, PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B. Buecow K.H., Schaefer C.F., Bhat N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peerers G.J., Abramson R.D., Mullahy S.J.,

Roares N.W., McEwan P.J., McKernan K.J., Malek J.A., Gunzarathe P.H.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Rahesley R.W., Touchman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Lakeeley R.W., Touchman J.W., Green B.D., Dickson M.C.,

RA Richards S.J., Marra M.A.,

RA Jones S.J., Marra M.J.,

RA Jones 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 BWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGNNGCDMGPDGRLLRGYHQHAYDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata; Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primateg, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 274; DB 2; Length 460; 100.0%; Pred. No. 4.6e-280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Strausberg R.; Strausberg R.; Strausberg R.; Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC009260. AAH09260.2; -. HSSP; Q29961; 1HSA. GO; GO:0016620; C::membrane; IEA. GO; GO:0016625; P::mmune response; IEA. InterPro; IPR007110; Ig-like. InterPro; IPR003997; Ig d. InterPro; IPR0030657; Ig d. InterPro; IPR003065; Ig MIC. InterPro; IPR001039; MHC. InterPro; IPR001039; MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 460 AA; 52263 MW; CIA0B6891978D93E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                  PRT; 460 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dest Docal Similarity 100.0%;
Matches 274; Conservative (
                                                                                                                                                                                         (TrEMBLrel. 19,
(TrEMBLrel. 26,
(TrEMBLrel. 26,
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ProDom; PD000050; MHC I; 1.
SMART; SM00407; IGC1; 1.
                                                                                                                                                                                                                                                                                             HLA-F protein (Fragment).
Name=HLA-F;
                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF07654; C1-set;
Pfam; PF00129; MHC I; 1
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                         01-DEC-2001
01-MAR-2004
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                                                                                                                                                                 095HC0;
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                                                                 RESULT 8
Q95HC0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 KDYISLNEDLKSWTAADTVAQITQRFYBABEYABBFRTYLBGBCLELLRRYLENGKETLQ 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGBEQTQDTELVETRPAGDGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RADPPKAHVAHHPISDHEATLRCWALGFYPABITLTWQRDGEBÖTGDTELVETRPAGDGT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EWITGYAKANAQIDRVALRNILRRYNQSEAGSHTLQGMNGCDMGPDGRILRGYHQHAYDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EWITGYAKANAQIDRVALRNILRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KDYISLNEDLRSWTAADTVAQITQRFYEAESYAESFRTYLEGGECLELLRRYLENGKETLQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XDYISLNEDLRSWTAADTVAQITQRFYEAEFYAEFFRTYLEGECLELLRRYLENGKETLQ 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAGDGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT 261
                                                                                                                                                                                             9
                                                                                                                                                                                                                                                    GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GSHSLRYFSTAVSRPGRGEPRY1AVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW
                                                                                                                                                                                                                                                                                                                     61 EWITGYAKANAQIDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDG
                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shiina T., Ota M., Katsuyama Y., Hashimoto N., Inoko H.; "Genome diversity in HLA: A new strategy for detection of genetic polymorphisms in expressed genes within the HLA class III and class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                 Length 362;
                                                             tch
100.0%; Score 274; DB 1; Length 36
al Similarity 100.0%; Pred. No. 3.7e-280;
274; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regions", submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases. Submitted (JUL-2002) BAC54915.1; -- SEQUENCE 362 AA; 40568 MW; BBDD041F920A34E1 CRC64;
362 AA; 40568 MW; B8DD041F820A34E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
Major histocompatibility complex, class I, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 FQKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POKWAAVVVPSGEEORYTCHVQHEGLPOPLILRW 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 AA.
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BAC54915;
   SEQUENCE
                                                             Query Match
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                                                                                            Local
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51 WVEQEGPQYWEWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLL 110
                       181 RADPPKAHVAHHPISDHEATLRCWALGFYPABITLITWQRDGEBQTQDTELVETRPAGDGT 240
                                                   202 RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 WVEQEGPQYWEWTTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 RGYHQHAYDGKDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 RGYHQHAYDGKDYISLNEDLRSWTAADTVAQITQRFYEAEBYAEBFRTYLEGECLELLRR 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 YLENGKETLQRADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTEL 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 YLENGKETLQRADPPKAHVAHHPISDHEATLRCWALGFYPABITLTWQRDGEEQTQDTEL 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pan troglodytes (Chimpanzee).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDIANE=21291697; PubMed=11398964;
Adams E.J., Parham P.;
"Genomic analysis of common chimpanzee major histocompatibility
complex class I genes.";
Immunoagenetics 53:200-208(2001).
EMBL; AF338355; AAK77479.1; -.
HSSP; Q29961; 1HSA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.8%; Score 224; DB 2; Length 346; 100.0%; Pred. No. 2.2e-227; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 VETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 VETRPAGDGTFOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pyo C.W., Ishitani A., Moore Y.F., Geraghty D.E.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. EMBL; AY64575, AAT13238.1; SEQUENCE 346 AA, 39082 MW; 6F739AA41917E7B2 CRC64;
                                                                                                                                                                                                                                                                                                                                  01-OCT-2004 (TrEMBLrel. 28, Created)
01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
MHC class Ib antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                         346 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 224, Conservative
                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                    241 FOKWAAVVVP 250
                                                                                                                                                                262 FOKWAAVVVP 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=HLA-F;
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                                                                                                                                                                     100 EWITGYAKANAQIDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGFDGRLLRGYHQHAYDG 159
                                                 KDYISINEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ 180
                                                                                       160 KDYISLNEDLRSWTAADTVAQITQRFYEAEBFRTYLBGECLELLRRYLENGKETLQ 219
                                                                                                                                           RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 EWTTGYAKANAQIDRVALKNILIRRYNQSEAGSHTLQGMNGCDMGPDGRILIRGYHQHAYDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 EWITGYAKANAQIDEVALENLIRRYNQSEAGSHILQGMNGCDMGPDGRLIRGYHQHAYDG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 KDYISINBDIRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLEILRRYLENGKETLQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 KDYISLNEDLRSWITAADIVAQIIQRFYEAEEFYATISGECLELLRRYLENGKETLQ 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREFWVEQEGPQYW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Ishitani A., Miki A., Williams L.M., Moore Y., Geraghty D.E.,
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
91.2%; Score 250; DB 2; Length 34:
Best Local Similarity 100.0%; Pred. No. 7.8e-255;
Matches 250; Conservative 0; Mismatches 0; Indels
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AF522284; AAM74991; --
EMBL; AF522291; AAM74996.1; --
EMBL; AF623292; AAM74997.1; --
EMBL; AY645748; AAT73231.1; --
EMBL; AY645749; AAT73237.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
MHC class Ib antigen.
                                                                                                                                                                                                                                        241 FOKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 274
                                                                                                                                                                                                                                                                                    280 FOKWAAVVVPSGEBORYTCHVQHEGLPQPLILKW 313
                                                                                                                                                                                                                                                                                                                                                                                                             346 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0016020; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:006955; P:immune response; IEA.
InterPro; IPR00310; Ig_c1.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003109; MHC.
Pfam; PF07654; C1-8et, 1.
Pfam; PF07654; C1-8et, 1.
PRMTS; PR01638; MHC.
PR01718; PR01638; MHC.
PR01718; PR01638; MHC.
PR01718; PS00030; MHC.
PR031718; PS00030; IG_MHC.
PR031718; PS00030; IG_MHC.
PR031718; PS00030; IG_MHC; 1.
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Best Local Similarity
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SMART; SM00407; IGC1; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
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                                                                                                                                                         Transmembrane
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0860R0
AC 0860R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 TIGYAKANAQTDRVALRNLIRRYNQSBAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDGKD 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 YISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQRA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 DPPKAHVAHHPISDHEATLRCWALGFYPAEITLITWQRDGEEQTQDTELVETRPAGDGTFQ 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 DPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAGDGTFQ 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22709134; PubMed=12799463;
Anzai T., Shina T., Kimura N., Yanagiya K., Kohara S., Shigenari A., Yamagira T., Khiski J.K., Naruse T.K., Pujimori Y., Fukuzumi Y., Yamazaki M., Tashiro H., Iwamoto C., Umehara Y., Imanishi T., Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H.;
"Comparative sequencing of human and chimpanzee MHC class I regions unveils insertions/deletions as the major path to genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0%; Pred. No. 1.7e-210;
Matches 208; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     346 AA; 39009 MW; 0ECF12B7DB17B814 CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
GO, GO:0016021; C:integral to membrane; IEA.
GO; GO:006955; P:immune response; IEA.
InterPro; IPR007110; IG-11ke.
InterPro; IPR003597; IG_C1.
InterPro; IPR003597; IG_C1.
InterPro; IPR003066; IG_MHC.
InterPro; IPR001039; MHC_I.
Pfam; PF00754; C1-set; 1.
Pfam; PF00754; MHC_I.
PR00103; MHC_I.
PR00103; MHC_I.
PR00103; PS000050; MHC_I; 1.
PR0011F; PS00035; IG_LIKE; 1.
PROSITE; PS00035; IG_LIKE; 1.
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 KWAAVVPSGEEQRYTCHVQHEGLPQPL 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 KWAAVVVPSGEEQRYTCHVQHEGLPQPL 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9598;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Patr-F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Class Ib
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                                                                                                                                                                                                63 TTGYAKANAQTDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDGKD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 DPPKAHVAHHPISDHEATLRCWALGFYPAEITLITWQRDGEEQTQDTELVETRPAGDGTFQ 263
                                                                                                                                                                                                                                       144 YISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQRA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 DPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGTFQ 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 EWTTGYAKANAQTDRVALRNILRRYNQSEAGSHTLQGMNGCDMGFDGRLLRGYHQHAYDG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 EWITGYAXANAQIDRVALRNILRRYNQSEAGSHILQGMNGCDMGPDGRLLRGYHQHAYDG 141
                                                                                                                                                                                                                                                                                                                                  123 YISLNEDLRSWTAADTVAQITQRFYEAZEYAEEFRTYLEGECLELLRRYLENGKETLQRA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 KDYISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 KDYISLNEDLRSWIAADTVAQITQRFYBAEBYABBFRIYLEGECLELLRRYLENGKETLQ 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 GSHSLRYFSTAVSRPGRGEPRYIAVETVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 81
                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                  ò
                                                      Query Match 75.9%; Score 208; DB 2; Length 362; Best Local Similarity 100.0%; Pred. No. 1.8e-210; Matches 208; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 3.7e-183;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu Y., He X., Xu L., Zeng Y.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AX253271; AAO86775.1; -.
GO; GO:00166952; Camembrane; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR001039; MHC_I.
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PRINTS; PR01638; MHCCLASSI.
ProDom; PD000050; MHC I; 1.
SEQUENCE 254 AA; 28588 MW; C81F225D409AAED2 CRC64;
362 AA; 40625 MW; BA5699D08181A1FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Name=Hish-Fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 254 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KWAAVVVPSGBEQRYTCHVQHEGLPQPL 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 KWAAVVVPSGEEQRYTCHVQHEGLPQPL 291
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 335:268-271(1988).
-!- FUNCTION: Involved in the presentation of foreign antigens to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHLA class I histocompatibility antigen, CH28 alpha chain.
Extracellular alpha-1.
Extracellular alpha-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).
                                                                                                   01-APR-1990 (Rel. 14, Last Sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA class I histocompatibility antigen, CH28 alpha chain precursor.
                                                                                                                                                                                        Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDIA 1990; MEDIA 1900; PubMed=3412487; MEDIA 1900; MADO 1900; PubMed=3412487; MADO 1900; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.0%; Score 126; DB 1; Length 346; 100.0%; Pred. No. 6.7e-124; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                      Lawlor D.A., Warren B., Ward F.E., Parham P.; "Comparison of class I MHC alleles in humans and apes."; Immunol. Rev. 113:147-185(1990).
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By similarity.
N-linked (GlCNAC. . .) (B)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00407; IGC1; 1.
PROSITE; PS50815; IG LIKE; 1.
PROSITE; PS00290; IG MHC; 1.
Glycoprotein; MHC 1; Signal; Transmembrane.
SIGNAL
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=90201944; PubMed=1690682;
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HASE; UKSTSI, ISTAIRE.
INTERPTO; IPR003597; IS_C1.
INTERPTO; IPR003065; IS_MHC.
INTERPTO; IPR001039; MHC_I.
Pfam; PP00129; MHC_I.
Pfam; PP00129; MHC_I.
Promy; PR0129; MHC_I.
Promy; PR0129; MHC_I.
                                                                              01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last seqn
01-APR-1993 (Rel. 25, Last anno
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                           STANDARD;
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204
204
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330
122
122
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103
346 AA;
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                        1C28 PANTR
P16215;
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TRANSMEM
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1C28_PANTR
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167 LLRRYLENGKETLORADPPKAHVAHHPISDHEATLRCWALGFYPAEITLTWORDGEEQTQ 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 LLRRYLENGKETLQRADPPKAHVAHHPISDHEATLRCWALGFYPABITLTWQRDGEEQTQ 161
84 TIGYAKANAQIDRVALRNLLRRYNQSEAGSHILQGMNGCDMGPDGRLLRGYHQHAYDGKD 143
                                     123 YISLNEDLRSWTAADTVAQITQRFYEAEEYAEEFRTYLEGECLELLRRYLENGKETLQRA 182
                                                        Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Pukuzumi Y., Pujimori Y., Komyyama M., Sugiyama T., Izie R., Cotsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y., Rawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekina M., Kikuchi H., Kanda K., Wagaftsuma M., Wurakawa K., Kanebori K., Takahashi-Pujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 DIELVETRPAGDGIFQKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 DIELVETRPAGDGIFOKWAAVVVPSGEEORYTCHVOHEGLPOPLILRW 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39.4%; Score 108; DB 2; Length 349; 100.0%; Pred. No. 6.9e-105;
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Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349 AA; 39039 MW; 5C00196F03393AA1 CRC64;
                                                                                                                                                                                                                                                                                  05-JUL-2004 (TERMBLrel. 27, Created)
05-JUL-2004 (TERMBLrel. 27, Last sequence update)
05-JUL-2004 (TERMBLrel. 27, Last annotation update)
Hypotherical protein FLJ41284.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. No. -
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Interpro; IPR007110; Ig-like.
Interpro; IPR003597; Ig-d.1.
Interpro; IPR003597; Ig-d.1.
Interpro; IPR003597; Ig-d.1.
Interpro; IPR001039; MHC_1.
Pfam; PF00407; Ig-d.1.
Pfam; PF00129; MHC_1.
ProDom; PD000050; MHC_1; I.
ProDom; PD000050; MHC_1; I.
PR0SITE; PS00835; IG_LIKE; I.
PR0SITE; PS00835; IG_LIKE; I.
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Matches 108; Conservative
                                                                                                                183 DPPKAH 188
                                                                                                                                                      204 DPPKAH 209
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                                                                                                                                                                                                               RESULT 15
OGZUWO
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Matches 126; Conservative

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: December 15, 2004, 18:13:46 ; Search time 28.0164 Seconds (without alignments)

941.000 Million cell updates/sec
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Title: Perfect score:	US-09-819-371-5 274
Sequence:	1 GSHSLRYFSTAVSRPGRGEPQRYTCHVQHEGLPQPLILRW
Scoring table: OLIGO	OTIGO

Gapop 60.0 , Gapext 60.0 asserted.

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2834;

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Listing first 45 summaries

Atabase : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		* Query			SUMMAKIES	
Š.	Score	Match	Length	DB	QI	Description
-	27		v	2	A60384	MHC class I histoc
7	3	ģ	4	~	807114	class I
m	73	è.	н	(7	C37028	class I
4	U O	21.5	348	~1	829990	npati
S		16.1	~	-4	HLHU10	MHC class I histoc
9	44	è.	6	~	S44994	ss I hist
٢	44	ø	Н	~	I36958	hla
Φ	44	16.1	N	7	I54449	class I
σ	44	16.1	m	~	S06424	class I
10	44	ø	4	~	I68749	lass I
11	44	è.	S	N	154551	осошра
12	44	ė.	S	7	I36966	lass I
13	44	9	5	N	136965	class I
14	44		2	н	HLHU12	MHC class I histoc
15	44		w	N	803535	class I histocompa
16	44	Ġ	φ	7	801171	a I hist
17	44	Ġ	9	~	136961	lass I
18	44		9	N	I37476	class I
13	44		9	N	A47636	1 88
20	44	ġ.	9	N	183063	2 - huma
21	44	16.1	9	N	156039	-A30.3
22	44	Ġ.	9	N	161856	class I
23	44	Ġ	9	7	137478	н
24	44	è.	9	~	I54493	class I
25	44		w	7	S77963	class I
56	44	ø	ø	N	138519	class I
27	44		9	(7)	I54416	Sro
28	44	16.1	9	N	138518	HLA-A-0102 allele
53	44		9	Н	HLHUW3	MHC class I histoc

MHC class I histoc	class I histocompa	lymphocyte antigen	MHC class I histoc	MHC class I histoc	lymphocyte antigen	MHC class I histoc		MHC class I histoc	MHC histocompatibi	MHC class I histoc	MHC class I histoc	MHC class I histoc	class I	MHC class I histoc	MHC class I histoc
I37526	JS0262	I81232	I38505	I37544	I81231	JH0526	I61866	137523	172113	168712	S42823	B37028	138507	137527	137135
N	N	7	~	0	7	7	~	N	N	N	~	7	~	~	7
366	366	366	366	366	366	366	366	366	366	366	366	366	366	366	366
16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1	16.1
	4	44	44	44	44	44	44	44	44	44	44	44	44	44	44
44	4														

ALIGNMENTS

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A; Molecule type: DNA
A; Residues: 1.362 cLUR>
A; Residues: 1.362 cLUR>
A; Cross-references: UNIPROT: P30511
B; Geraghty, D.E.; Wel, X.; Orr, H.T.; Koller, B.H.
J. Exp. Med. 171, 1-18, 1990
J. Exp. Med. 171, 1-18, 1990
A; Title: Human leukocyte antigen F (HLA-F): an expressed HLA gene composed of a class I A; Reference number: Ju0147; MUID: 90111605; PMID: 1688605
A; Accession: JL0147
MHC class I histocompatibility antigen HLA-F alpha chain Dew3 precursor - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1993 #text_change 09-Jul-2004
C;Date: 03-Mar-1993 #text_change 09-Jul-2004
C;Accession: A60384; Jul0147
R;Lury, D.; Epstein, H.; Holmes, N.
Int. Immunol. 2, 531-237, 1990
A;Title: The human class I MHC gene HLA-F is expressed in lymphocytes.
A;Reference number: A60384; MUID:91197689; PMID:1707659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 EWITGYAKANAQIDRVALRNILRRYNQSEAGSHILQGNNGCDMGPDGRLLRGYHQHAYDG 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDŢQFLRFDSDAAIPRMEPREPWVEQEGPQYW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 GSHSLRYFSTAVSRPGRGEPRYIAVEYVDDTQFLRFDSDAAIPRMEPREPWVEQEGPQYW 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A/CHECOMEST CONTINUATION OF THE ALGORITHM OF THE ALGORITH
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A;Residues: 1-562 cGER>
A;Cross-references: GB:XI7093; NID:G32223; PIDN:CAA34947.1; PID:G312407
A;Experimental source: lymphoblastoid cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 274; DB 2; Length 362;
Best Local Similarity 100.0%; Pred. No. 1.1e-282;
Matches 274; Conservative 0; Mismatches 0; Indels 0
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C;Accession: B24512
R;Davidson, W.F; Kress, M.; Khoury, G.; Jay, G.
B. Biol. Chem. 260, 13414-13423, 1985
A;Title: Comparison of HLA class I gene sequences. Derivation of locus-specific oligonucl
A;Reference number: A92500, MUID:86033791; PMID:3863816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Cross-references: UNIPROT:P33617; EMBL:Z21819; NID:g38568; PIDN:CAA79885.1; PID:g38569
C,Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: transmembrane protein
F;219-284/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: UNIPROT:P01892; GB:M11887; NID:9184157; PIDN:AAA52656.1; PID:9184158
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A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen
F:130-195/Domain: immunoglobulin homology <IMM>
F:20/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                     169 SDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGTFQKWAAVVVPSGSE 228
      195 SDHEATLRCWALGFYPAEITLTWQRDGEEQTQDTELVETRPAGDGTFQKWAAVVVPSGEE 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 BITLIWQRDGEEQTQDTELVETRPAGDGTFQKWAAVVVPSGBEQRYTCHVQHEGLPQPL 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 BIILTWQRDGEBQTQDTELVETNPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLPQPL 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WHC class I histocompatibility antigen HLA-AlO alpha chain - human (fragment)
                                                                                                                                                                                                                                                                                                                                              histocompatibility antigen, HLA-F-like - rhesus macaque (Species: Macaca mulatta (rhesus macaque) (Cispecies: Macaca mulatta (rhesus macaque) (Cispecies: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004 (Ciscossion: 82999) R;Bontrop, R.R. Ribontrop, R.R. Bubl. Data Library, February 1993 A;Reference number: $29990 A;Accession: $29990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                class I histocompatibility antigen HLA-Cw6 precursor - human (fragment)
C,Species: Homo sapiens (man)
C,Date: 13-Jan-1995 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 348;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 QIQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.5%; Score 59; DB 2; Le
100.0%; Pred. No. 2.5e-54;
iive 0; Mismatches 0;
                                                                                                                                 255 QRYTCHVQHEGLP 267
                                                                                                                                                                                           229 ORYTCHVOHEGLP 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 59; Conservative
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A; Residues: 1-275 < DAV>
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A; Residues: 1-348 <BON>
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R;Cianetti, L.; Testa, U.; Scotto, L.; La Valle, R.; Simeone, A.; Boccoli, G.; Giannella Immunospenetics 29, 80-91, 1989
A;Title: Three new class I HLA alleles: structure of mRNAs and alternative mechanisms of A;Reference number: A37028; MUID:89122144; PMID:2914713
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                                                                                                                                                                                                                                                                                                                                                                                                                                          WHC class I histocompatibility antigen Ch28 alpha chain precursor - chimpanzee C; Species: Pan troglodytes (chimpanzee) C; Species: Pan troglodytes (chimpanzee) C; Species: Pana-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000 C; Accession: S07114 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000 R; Lawlor, D.A.; Ward, F.E.; Ennis, P.D.; Jackson, A.P.; Parham, P. Nature 335, 268-271, 1988 A; Filtle: HLAA and B polymorphisms predate the divergence of humans and chimpanzees. A; Reference number: S06424; MUID:88319000; PMID:3412487
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                                                                                                   RADPPKAHVAHHPISDHEATLRCWALGFYPAEITLIWQRDGEEQTQDTELVETRPAGDGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 ITGYAKANAQIDRVALRNLLRRYNQSEAGSHTLQGMNGCDMGPDGRLLRGYHQHAYDGKD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 TIGYAKANAQIDRVALRNILRRYNQSEAGSHILQGMNGCDMGPDGRLLRGYHQHAYDGKD 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YISLNEDLRSWIAADTVAQITQRFYBAEEYAEBFRIYLEGECLELLRRYLENGKETLQRA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 YISLNEDLRSWTAADTVAQITORFYEAEEFYAFEFFTYLEGGCLELLRRYLENGKETLQRA 203
142 KDYISLNEDLRSWTAADTVAQITQRFYEAESYAEBFRTYLEGECLELLRRYLENGKETLQ 201
                                                                                                                                                                202 RADPPKAHVAHHPISDHEATLRCWALGFYPABITLTWQRDGEEQTQDTELVETRPAGDGT 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Homo sapiens (man)
Date: 14-Feb-1992 #sequence_revision 30-Jan-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mrnà
Residues: 1-345 < LiAW>
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Keywords: glycoprotein; membrane protein
F;217-282/Domain: immunoglobulin homology < LMM>
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C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;170-235/Domain: immunoglobulin homology <1MM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.6%; Score 73; DB 2; Length 316; ilarity 100.0%; Pred. No. 3s-69; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                      262 FQKWAAVVVPSGEEQRYTCHVQHEGLPQPLILRW 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 126; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DPPKAH 209
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Best Local Similarity
Matches 73; Conserv
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A, Molecule type: mRNA
A, Residues: 1-316 <CIA>
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C;Accession: 168749

R;Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.

R;Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.

R;Pohla, H.; Kuon, W.; Tabaczewski, P.; Doerner, C.; Weiss, E.H.

A;Title: Allelic variation in HIA-B and HIA-C sequences and the evolution of the HIA-B a

A;Reference number: 154487; WUID:89233295; PMID:2714852

A;Accession: 168749
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A;Molecule type: mRNA
A;Residues: 1-345 <RBS.
A;Cross-references: UNIPROT:Q29963; GB:M28206; NID:g576476; PIDN:AAA57258.1; PID:g576477
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;199-264/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                              MHC class I histocompatibility antigen Ch25 alpha chain precursor - chimpanzee NAC ch1A chain c)Species: Pan troglodytes (chimpanzee) C;Species: Pan troglodytes (chimpanzee) C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004 C;Accession: S06424; 136959 R;Lawlor, D.A.; Ward, F.E.; Ennis, P.D.; Jackson, A.P.; Parham, P. Nature 335, 268-271, 1998 A;Ritle: HIA-A and B polymorphisms predate the divergence of humans and chimpanzees. A;Reference number: S06424; MUID:88319000; PMID:3412487
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C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Molecule type: mRNA
A, Residues: 1-33 cRES.
A, Residues: 1-33 cRES.
A, Crose-references: Gs. M24047; NID: g176818; PIDN: AAA35426.1; PID: g553155
C, Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Keywords: glycoprotein; membrane protein
C; Keywords: glycoprotein; membrane protein
C; Keywords: glycoprotein; membrane protein
F; 124 Chomain: alpha-1 #status predicted < KIG.
F; 124 Chomain: alpha-1 #status predicted < KIZ.
F; 126 Commain: alpha-2 #status predicted < KIZ.
F; 120 CBS (Domain: immunoglobulin homology < IMM.
F; 1070-331 (Domain: transmembrane #status predicted < TWM.
F; 110 (Mainding site: carbohydrate (Asn) (covalent) #status predicted
F; 125-188, 227-283/ Disulfide bonds: #status predicted
                                            Gaps
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                                                                                                              · 224 QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 267
                                                                                                                                                   207 QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 250
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           1 Similarity 100.0%; Pred. No. 2e-38; 44; Conservative 0; Mismatches 0; Indels
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A,Residues: 1-332 -LAM>
A,Fesidues: 1-332 -LAM>
A,Cross-references: UNIFROT.030990
R;Parham, P.; Lawlor, D.A.; Lomen, C.B.; Ennis, P.D.
A,Immunol. 142, 3937-3950, 1989
A;Title: Diversity and diversification of HIA-A,B,C alleles.
A,Reference number: 136956; MUID:89235215; PMID:2715640
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100.0%; Pred. No. 2.1e-38;
tive 0; Mismatches 0;
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100.0%; Pred. No. 2e-38;
ive 0; Mismatches (
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Matches 44; Conservative
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           Best Local Similarity
Matches 44; Conserv
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C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;1-72/Domain: signal sequence #setatus predicted <SIG>
F;73-298/Product: class I histocompatibility antigen HLA-CW6 (fragment) #status predicte
F;220-285/Domain: immunoglobulin homology <IMM>
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C,Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;167-232/Domain: immunoglobulin homology <IMM>
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Immunogenetics 28, 265-270, 1988
A; Title: Cloning and analysis of HLA class I cDNA encoding a new HLA-C specificity Cx52.
A; Reference number: I54449; MUID:88330144; PMID:2843461
A; Accession: I54449
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C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jan-2000
C;Accession: 154449
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C;Species: Pan troglodytes (chimpanzee)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
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C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;179-244/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R.Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D. J. Immunol. 142, 3937-3950, 1989.
A.Title: Diversity and diversification of HLA-A,B,C alleles. A;Reference number: 136956; MUID:89235215; PMID:2715640
A;Accession: 136958
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100.0%; Pred. No. 1.8e-38;
tive 0; Mismatches 0;
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A;Molecule type: mRNA
A;Residues: 1-325 <RES>
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A;Molecule type: mRNA
A;Residues: 1-313 <RES>
C,Accession: S44994
R;Marget, M.; Brockstedt, D.; Jenisch, S.
submitted to the EmBL Data Library, May 1994
A;Description: New HLA-CM6 Sequence.
A;Reference number: S44994
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Best Local Similarity
                                                                                                                                                                         A; Accession: S44994
A; Molecule type: mRNA
A; Residues: 1-298 < MAR>
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R; Parham, P.; Lawlor
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224 QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 267

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16.1%; Score 44; DB 2; Length 325;

Query Match

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A;Cross references: UNIPROT:Q9MXL1; UNIPROT:Q30992; GB:M55244; NID:g176834; PIDN:AAA72082
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;212-277/Domain: immunoglobulin homology <1MM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MHC class I histocompatibility antigen HLA alpha chain precursor (clone pHLA 12.4) - hums
C;Species: Homo sapiens (man)
C;Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 class I histocompatibility antigen ChLA-A108 alpha chain precursor - chimpanzee (fragment
C;Species: Pan troglodytes (chimpanzee)
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: S03535
R;Mayer, W.B.; Jonker, M.; Klein, D.; Ivanyi, P.; van Seventer, G.; Klein, J.
BMBO J. 7, 2765-2774, 1988
A;Title: Nuclectide sequences of chimpanzee MHC class I alleles: evidence for trans-spec:
A;Reference number: S01171; MUID:89030641; PMID:2460344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:J00191; GB:V00526; NID:g187600; PIDN:AAA36218.1; PID:g386873 C;Comment: The seven exons correspond approximately to the domain structure of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Malissen, M.; Malissen, B.; Jordan, B.R.
Proc. Natl. Acad. Sci. U.S.A. 79, 893-897, 1982
A;Title: Exon/intron organization and complete nucleotide sequence of an HLA gene.
A;Reference number: A02189; MUID:82151002; PMID:6461010
                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                       224 QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 267
                                                                                                                                                                                                                                                                                                                 240 QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 OTODÍELVETRPAGDGIFOKWAAVVVPSGEEORYÍCHVOHEGLP 288
                                                                                                                                                                                                              0; Indels
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                                                                                                                                           Ouery Match
Best Local Similarity 100.0%; Pred. No. 2.2e-38;
Matches 44; Conservative 0; Mismatches 0;
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16.1%; Score 44; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 2.2e-38;
Matches 44; Conservative 0; Mismatches 0;
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A; Residues: 1-359 < MAL>
      A;Residues: 1-357 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A02189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q95513; EMBL:U02976; NID:g413827; PIDN:AAA70050.1; PID:g413$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mzna
A;Residues: 1-357 <RES>
A;Cross-references: UNIPROT:Q9MXL2; UNIPROT:Q30993; GB:M55245; NID:g176836; PIDN:AAA0368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Accession: 136966
R,Chen, Z.W.; Hughes, A.L.; Ghim, S.H.; Letvin, N.L.; Watkins, D.I.
R,Chen, Z.W.; Hughes, A.L.; Ghim, S.H.; Letvin, N.L.; Watkins, D.I.
A;Title: Two more chimpanzee Patr. A locus alleles related to the HLA-Al/A3/All family.
A;Reference number: 136965; MUID:93279743; PMID:8505066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyaccession: 136965 Forthway A.L.; Ghim, S.H.; Letvin, N.L.; Watkins, D.I.
Richen, Z.W.; Hughes, A.L.; Ghim, S.H.; Letvin, N.L.; Watkins, D.I.
Immunogenetics 38, 238-240, 1993
A; Title: Two more chimpanzee Patr-A locus alleles related to the HLA-A1/A3/A11 family.
A; Reference number: 136965; MUID: 93279743; PMID: 8505066
A; Accession: 136965, A; Annalated from GB/EMBL/DDBJ
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                                                                                                                                                                           histocompatibility antigen - crab-eating macaque (fragment)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MHC class I protein - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
C;Date: 04-0ct-1996 #sequence_revision 04-0ct-1996 #text_change 09-Jul-2004
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C;Species: Pan troglodytes (chimpanzee)
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
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C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;212-277/Domain: immunoglobulin homology <IMM>
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227 QIQDIELVETRPAGDGTFQKWAAVVVPSGEEQRYICHVQHEGLP 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 QIQDTBLVETRPAGDGTFQKWAAVVVPSGBEQRYTCHVQHBGLP 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary, translated from GB/EMBL/DDBJA;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity
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Best Local Similarity
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F;219-284/Domain: immunoglobulin homology <IMM>
F;298-336/Domain: transmembrane #status predicted <TMM>
F;337-364/Domain: intracellular #status predicted <INT>
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Query Match 16.1%; Score 44; DB 2; Length 364; Best Local Similarity 100.0%; Pred. No. 2.2e-38; Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps

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Search completed: December 15, 2004, 18:25:17 Job time: 29.0164 secs

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December 15, 2004, 18:14:01; Search time 30.818 Seconds (without alignments) 589.627 Million cell updates/sec
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274
1 GSHSLRYFSTAVSRPGRGEP......QRYTCHVQHEGLPQPLILRW 274
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1: /cgT2_6/ptodata1/iaa/5A_COMB.pep:*
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6: /cgD2_6/ptodata1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                      478139 seqs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Listing first 45 summaries
                                                                                    OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 4290, Appsequence 1, Appli Sequence 9, Appli Sequence 8, Appli Sequence 9, Appli Sequence 109, Appli Sequence 109, Appli Sequence 100, Appli Sequence 99, Appli Sequence 90,	מלחבוורם אזי
SUMMARIES	US-09-513-999C-4290 US-08-222-881-1 US-08-406-057-9 US-08-958-116-9 US-08-958-116-9 US-08-958-116-9 US-08-958-116-9 US-08-958-116-9 US-08-484-905-105 US-08-484-905-105 US-08-484-905-105 US-08-484-905-105 US-08-484-905-106 US-08-370-476-108 US-08-370-476-108 US-08-370-476-108 US-08-370-476-109 US-08-484-905-99 US-08-484-905-99 US-08-484-905-99 US-08-481-9958-99	6-900-TOF-00-
DB	4-14-14-14-14-14-14-14-14-14-14-14-14-14	1
Length	11011111100000000000000000000000000000	
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Score	₩ # # # # # # # # # # # # # # # # # # #	,
Result No.	44887888888888888888888888888888888888	

Sequence 100, App Sequence 23, Appl Sequence 23, Appl Sequence 27, Appl Sequence 97, Appl Sequence 97, Appl Sequence 100, App Sequence 101, Appl Sequence 101, Appl Sequence 83, Appl Sequence 83, Appl Sequence 83, Appl Sequence 84, Appl Sequence 82, Appl Sequence 80, Appl	Encoded Human Proteins.	i Length 120; 0; Indels 0; Gaps 0; 0; Indels 0; Gaps 0; EDSDAAIPRMEPREPWVEQEGPOYW 60 FDSDAAIPRMEPREPWVEQEGPOYW 81 CGWN 99 CGWN 120	E ("CTL")
3 US-08-481-985B-100 3 US-08-481-985B-101 3 US-08-384-497A-23 3 US-08-370-476-97 3 US-08-370-476-98 3 US-08-370-476-98 3 US-08-370-476-100 3 US-08-370-476-101 3 US-08-484-905-82 4 US-08-484-905-82 5 US-08-484-905-80	ALIGNMENTS 9513999C , J.B. Sequence Tags and /09/513,999C 24 0/122,487	Score 99; DB 4 1; Pred. No. 2e-9 0; Mismatches SEPRYIAVEVVDDTOFIR	ALMAN M. PETER CYTOTOXIC T-CELL LYMPHOCYTE ("CTL")
100.6 100.6	-999C-4290 No. 673961 INFORMATION: ANT: Dumas Milne Edw ANT: Duclert, A. ANT: Giordano, J.Y. OF INVEXTION: Expres No. 6739961 EFERENCE: 59.US2.REG T PELING DATE: 2000 APPLICATION NUMBER: FILING DATE: 1999-02 OF SEQ ID NOS: 3668 RE: Patent.pm H: 120 PRT HI 120 PRT HISH Homo sapiens RE: SIGNAL INNORMATION: seq SL- 100N: -171 INFORMATION: seq SL-	Match Local Similarity 100.03 es 99; Conservative 1 GASSLENYESTAVSEPGRC	: NAENSAI, PETE : PARHAM, PETE INVENTION: CYT
80000000000000000000000000000000000000	RESULT 1 US-09-513-999C-4290 Sequence 4290, Application US/0 Patent No. 6783961 GENERAL INFORMATION: APPLICANT: Dumas Milne Edwards APPLICANT: Dumas Milne Edwards APPLICANT: Giordano, J.Y. ITILE OF INVENTION: Expressed PATENT OF INFORMING: EDWARD: CURRENT APPLICATION NUMBER: US CURRENT FILING DATE: 1999-02-26 NUMBER OF SEQ ID NOS: 36681 SOFTWARE: PATENT FILING DATE: 1999-02-26 NUMBER OF SEQ ID NOS: 36681 SOFTWARE: PATENT FILING DATE: 1999-02-6 NUMBER OF SEQ ID NOS: 36681 SOFTWARE: RENT FILING DATE: 1999-02-76 NUMBER OF SEQ ID NOS: 36681 SOFTWARE: RENT FILING DATE: 1999-02-76 NUMBER OF SEQ ID NOS: 36681 SOFTWARE: RENT CORPANIES: NAME/KEY: SIGNAL LOCATION: -171 COTHER INFORMATION: SEQ SLILLLL US-09-513-999C-4290	Query Match Best Local Similarity Matches 99; Conservat OY 1 GSHSLRYFSTAV OY 61 EWTTGYAKANA, OY 61 EWTTGYAKANA, Db 82 EWTTGYAKANA, TS-08-22-851-1 'S Sequence 1, Application 'S SEGUENCE 1, APPLICANT. 'S SEGUENCE 1,	HALL

Gaps

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Sequence 9, Application US/08958316

Sequence 9, Application US/08958316

CENERAL INFORMATION:
APPLICANT: CAROSELLA, EDGARDO D
APPLICANT: MCREAL WHILEPE
APPLICANT: MCREAL WHILEPE
APPLICANT: MCREAL WANGERIER
APPLICANT: TRANSCRIPTS
TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLOW, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1155 S. JEFFERSON DAVIS HIGHMAY, FOURTH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cuery Match
14.2%; Score 39; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 6.3e-31;
Matches 39; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
T: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
ARLINGTON
: VIRGINIA
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 ELVETRPAGDGTFOKWAAVVVPSGEEORYTCHVOHEGLP 267
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RILING DATE: 27-0CT-1997
CLASSIPICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FF 94 03179
FILING DATE: 18-MAR.1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 0846-043
TELECHOMONICATION INFORMATION:
TELEFAX: (703) 413-220
TELEFAX: (703) 413-200
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN P
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 846-7
TELECHONICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFX: 748855 OPAT UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
                                                                                                                                                                                                                                                                                                      LENGTH: 117 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear NOLECULS TYPE: peptide US-08-406-057-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
     TITLE OF INVENTION: ACTIVITY REGULATION BY CLASS I MHC PEPTIDES NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORALSON & FOERSTER STREET: 2000 PENNSYLVANIA AVENUE, NW, STE 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 16.1%; Score 44; DB 1; Length 274; Best Local Similarity 100.0%; Pred. No. 1.5e-35; Matches 44; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/08406057
Patent No. 5856442
GENERAL INFORMATION:
APPLICANT: CARCSELLA, EDGARDO D
APPLICANT: GLUCKMAN, ELLANE
APPLICANT: GLUCKMAN, ELLANE
APPLICANT: GLUCKMAN, ELLANE
APPLICANT: GLUCKMAN, ELLANE
APPLICANT: AFRANSCRIPTS OF THE MHC CLASS I HLA-G
TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSED: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR STATE: VIRGINIA
STATE: VIRGINIA
STATE: VIRGINIA
GOUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 QTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 OTODIELVETRPAGDGTFOKWAAVVVPSGEEORYTCHVQHEGLP 267
                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPY disk

COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATIC SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: PATENT NO NUMBER: US/08/22,851
FILING DATE: 05-APR-1994
ATTONENT/AGENT INFORMATION:
NAME: MILLMAN, ROBERT A.
REGISTRATION NUMBER: 36,217
REFERENCE/POCKET NUMBER: 36,217
REFERENCE/FOCKET NUMBER: 36,217
RELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 494-0792
TELEPHONE: 274 AMAIO ACID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 274 AMAIO ACID
TYPE: AMAIO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER REAUGHT.

MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/406,057
TTING DATE: 17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FR 94 03179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
US-08-222-851-1
                                                                                                                                          WASHINGTON
                                                                                                                                                                                                    USA
                                                                                                                                             CITY: WAS
STATE: D
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
US-08-406-057-9
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CAROSELLA, EDGARDO D
MOREAU, PHILIPPE
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 2202
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-484-905-79
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                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: OROSELLA, EDGARDO D
APPLICANT: OROSELLA, PHILIPPE
APPLICANT: OROSELLA, PHILIPPE
APPLICANT: MIREAU
APPLICANT: KIREZERBAUM, MAREK
TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
STATE: VIRGINIA
COUNTRY: USA
                                                  Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 145;
                                               Ouery Match
14.2%; Score 39; DB 3; Length 117
Best Local Similarity 100.0%; Pred. No. 6.3e-31;
Matches 39; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
COPETATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,057
FILING DATE: 17-MAR-1995
CLASSIFICATION DATA:
PRICE APPLICATION DATA:
REPLICATION NUMBER: FR 94 03179
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLOW, NORMAN F
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REFERENCE/POCKET NUMBER: 24,618
REFERENCE/POCKET NUMBER: 331-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                               229 ELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 ELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 267
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                                                                                                                                                                                          51 ELVETRPAGDGTFOKWAAVVVPSGEEORYTCHVOHEGLP 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

14.2%; Score 39; DB 2; De
Best Local Similarity 100.0%; Pred. No. 7.6e-31;
Matches 39; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08406057
Patent No. 5856442
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703) 413-2220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 8:SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 145 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 2202
COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-08-406-057-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
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                                                                                                                                                                                                                                                                                            -08-406-057-8
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US-08-958-316-8
US-08-958-316-9
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Sequence 79, Application US/08484905
Patent No. 597651
GENERAL Incomation
GENERAL Incomation
GENERAL Incomation
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Convilatorial Description
TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Using the
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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APPLICANT: MOREAU, PHILIPPE
APPLICANT: GUCKMAN, ELIANE
APPLICANT: GUCKMAN, ELIANE
APPLICANT: GUCKMAN, LIANE
APPLICANT: GUCKMAN, MARSKRIPTS OF THE MHC CLASS I HLA-G
TITLE OF INVENTION: TRANSCRIPTS OF THE MHC CLASS I HLA-G
TITLE OF INVENTION: GENE AND THEIR APPLICATIONS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
CITY: ARLINGANIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
14.2%; Score 39; DB 3; Length 145;
Best Local Similarity 100.0%; Pred. No. 7.6e-31;
Matches 39; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFOURER: Table Form:

MEDIUM TYPE: Tabe
COMPOUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: D40/06/958,316
FILING DATE: 27-OCT-1997
CRIASSIFICATION DATA:
APPLICATION NUMBER: FR 94 03179
FILING DATE: 18-MAR-1994
FILING DATE: 18-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN P
REFERENCE/DOCKET NUMBER: 0846-0437-0
TELEPHONE: (703) 413-220
TELEPHONE: (703) 413-320
TELEPHONE: (703) 413-320
TELERX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LUMBER: LABBER OF ALCOMENTION: AND ALCOMENTION OF ALCOMENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 ELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLP 117
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 79, Application US/08481985B
Patent No. 601146
GENERAL INFORMATION:
APPLICANT: Abstado, bean-pierre
APPLICANT: Abstado, bean-pierre
APPLICANT: Kourilsky, Phillipe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 10.9%; Score 30; DB 2; Length 289; Best Local Similarity 100.0%; Pred. No. 1.2e-21; Matches 30; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
                                            CORFACTION STSTEM:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

CLASSIFICATION DATA:

APPLICATION DATA:

CLASSIFICATION DATA:

APPLICATION DATA:

CLASSIFICATION DATA:

APPLICATION NUMBER: US 07/792,473

APPLICATION NUMBER: US 07/792,473

APPLICATION: 530

CLASSIPICATION: 530

ATONNEY/AGENT INPORMATION:

NAME:

REGISTRATION NUMBER: 33,332

REBERBENCE/DOCKET UNBER: 33,332

REBERBENCE/DOCKET UNBER: 33,332

REBERBANCE/DOCKET UNBER: 33,332

REBERBANCE/DOCKET UNBER: 33,332

REBERBANCE/DOCKET UNBER: 31,332

REBERBANCE/DOCKET UNBER: 31,332

REBERBANCE/DOCKET UNBER: 31,332
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STATE: D.C.
STATE: D.C.
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,985B
FILING DATE: 07-JUN-1995
CLASSIFICATION 435
PRIOR PAPLICATION ATA:
FILING DATE: 05-DEC-1991
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 QDTELVETRPAGDGTFQKWAAVVVPSGEEQ 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 ODTELVETRPAGDGTFOKWAAVVVPSGEEO 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS-/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-905-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-481-985B-79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
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ATTORNEY/JEANT TRIPORATION:
NAME: TRIPORATION:
NAME: 25,146
REPERENCE/DOCKET NUMBER: 3,146
REPERENCE/DOCKET NUMBER: 3,147
REPERENCE/DOCKET NUMBER: 3,147
REPERENCE/DOCKET NUMBER: 3,147
RE
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224 QTQDTELVBTRPAGDGTFQKWAAVVVPSG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 274 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide US-08-484-905-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                         RESULT 11
US-08-484-905-107
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Jeguence 105, Application US/08484905

Patent No. 59765105

Patent No. 59765105

APPLICANT: Mottez, Estelle

APPLICANT: Mottez, Estelle

APPLICANT: Abastado, Jean-Pierre

APPLICANT: Abastado, Determinant and Methods for Using the

TITLE OF INVENTION: Complex (MHC) Determinant and Methods for Using the

TITLE OF INVENTION: Determinant

NUMBER OF SEQUENCES: 127

CORRESPONDENCE ADDRESS:

ADDRESSEE: FILINGATION N.W., Suite 700

CITY: Washington

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STREET: 1300 I Street, N.W., Suite 700

CITY: Washington

STREET: Ploppy Disk

COMPUTER: IBM PC Compatible

OPERATING STREE: Ploppy Disk

COMPUTER: Determinant Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 07/801,818

FILING DATE: 05-DEC-1991

CLASSIFICATION NUMBER: US 07/792,473

FILING DATE: 15-NOV-1991

CLASSIFICATION NUMBER: 15-NOV-1991

CLASSIFICATION NUMBER: 15-NOV-1991

FILING DATE: 15-NOV-1991
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10.9%; Score 30; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 30; Conservative 0; Mismatches 0;
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ATTORNEY/AGENT INFORMATION:
NAME: POCLER, Jane B. R.
REGISTRATION NUMBER: 33,332
REPERNCK/DOCKET NUMBER: 0349:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
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INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
LENGIH: 274 anino acids
     INFORMATION FOR SEQ ID NO: 79:
                                         LENGTH: 289 amino acids
TYPE: amino acid
TOPCLOGY: linear
MOLECULE TYPE: peptide
US-08-370-476-79
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amino acid
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Best Local Similarity 100.0
Matches 29; Conservative
                              SEQUENCE CHARACTERISTICS:
LENGTH: 289 amino acid
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224 QTQDTELVETRPAGDGTFQKWAAVVVPSG 252

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APPLICANT: Mottez, Estelle
APPLICANT: Mostez, Gen-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: An Altered Major Histocompatibility
TITLE OF INVENTION: Complex(WHC) Determinant and Methods for Using the
TITLE OF INVENTION: Determinant
NUMBER OF SEQUENCES: 127
CORRESPONDENCE 127
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10.6%; Score 29; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 29; Conservative 0; Mismatches 0; Indels
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Patent No. 5976551
GENERAL INFORMATION:
APPLICANT: Motez, Estelle
APPLICANT: Abastado, dean-plerre
APPLICANT: Abastado, ban-plerre
APPLICANT: Abastado, ban-plerre
APPLICANT: Abastado, Aballippe
APPLICANT: An Altered Major Histocompatibility
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CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
TILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/792,473
ATING DATE:
APPLICATION:
ANAME:
APPLICATION:
ANAME:
APPLICATION:
ANAME:
APPLICATION NUMBER:
APPLICATION APPLICAT
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STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
MEDIUM TYPE: TIBM PC compatible
".v.pitter: TIBM PC COMPATIBLE
".v.
Sequence 107, Application US/08484905
Patent No. 5976551
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INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
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US-08-481-985B-105
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US-08-481-985B-107
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TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the TITLE OF INVENTION: Determinant NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
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| Sequence 105, Application US/08481985B
| Patent No. 6011146|
| Patent No. 6011146|
| APPLICANT: Mortez, Estelle
| APPLICANT: Mourilaky, Phillipe
| TITLE OF INVENTION: Altered Major Histocompatibility Complex TITLE OF INVENTION: Altered Major Histocompatibility Complex CORRESPONDENCES: 148
| CORRESPONDENCES: 148
| CORRESPONDENCES: Pinnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner | ADDRESSEE: Dunner | ADDRESSEE: Dunner | ADDRESSEE: Dunner | ADDRESSEE: STREET: 1300 | Street, N.W., Suite 700 | STREET: 1300 | Street, N.W., Suite 700 | STREET: STREET:
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10.6%; Score 29; DB 2; Length 274;
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 29; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                      ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                         CITY: WASTINGTON
STATE: D.C.

ZIP: 20005-3315
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS-/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,905
FILING DATE: 07-JUNE 1995
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INPORMATION:
NAME: POLICEY, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 03495.0106-03000
TELECOMMUTCATION INPORMATION:
THE ERPONE: 202-408-4000
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1300
TTY: Washington
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Septembran, Septemin Ralasse #1.0, Version #1.25

CURRETA APPLICATION NATA:

APPLICATION NATA:

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APPLICATION NATA
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BD187421 Cancer cell
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CQ776417 Sequence
CQ776511 Sequence
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AX21682 Homo sapi
AX21684 Cancer cell
AX52556 Sequence
CQ72214 Sequence
E63815 Cancer pr
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
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CQ776417
AY253270
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length DB
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E63813 1089 bp DNA linear PAT 27-AUG-2002 Cancer cell-specific HLA-F antigen and method for diagnosing cancer

LOCUS DEFINITION

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Cancer cell-specific HLA-F antigen and method for diagnosing cancer
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GOLN33/53, GOLN33/574, GOLN33/68// (CL2N1/21, CL2R1:19), (CL2P21/02, PC
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: JP 2001095584-A 1 10-APR-2001;
KOJI BGAWA,KK MEDINET,KEIJI KIMURA
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/mol_type≈"genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                Homo sapiens (human)
JP 201095584-A/1
10-APR-2001
30-SEP-1999 JP 1999279566
KOJI BGAWA
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                 E63813.1 GI:22553651 JP 2001095584-A/1.
                                                           Homo sapiens (human)
Homo sapiens
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Matches 1089; Conservative
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pulmonary disease
Patent: EP 1394274-A 197 03-MAR-2004;
Genox Research, Inc. (JP)
Location/Qualifiers
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Sequence 197 from Patent EP1394274.
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/mol_type="unassigned DNA"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Patent: EP 1394274-A 103 03-MAR-2004;
Genox Research, Inc. (JP)
Location/Qualifiers
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Sequence 103 from Patent EP1394274.
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/organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
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            601 CAGCGCGCAGATCCTCCAAAGGCACACGTTGCCCACCACCCATCTCTGACCATGAGGCC
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Homosapiens MHC class Ib antigen (HLA-F) mRNA, HLA-F*0101 variant 2 allele, complete cds.
A7253270
A7253270.1 GI:29650892

DEFINITION ACCESSION VERSION

RESULT 6 AY253270 LOCUS

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 1041)

1 (bases I to 1041)

1 (Louing of full-length HLA-F*0101 variant 2 cDNA from Han Chinese Unpublished

2 (bases I to 1041)

2 (bases I to 1041)

Direct Submission

Submitted (GB-MAR-2003) Key Laboratory of Ministry of Education for Submitted (GB-MAR-2003) Confirm and Immunology, Jinan University, Shipai, Guangzhou, Guangdong 510632, China

Location/Qualifiers
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note="non-classical; similar to HLA-F*0101 but lacks exon
; alternatively spliced"
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/cell type="peripheral leukocytes"
/cev gtage="adult"
1. .1041
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/db_xref="taxon:9606"
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\allele="HLA-F*0101 variant 1"
/note="non-classical; similar to HLA-F*0101 but lacks exon
7; alternatively spliced"
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AVEYVDDTQFLRFDSDAAIPRMEPREPWYEGEZPQYWEWTTGYKANAQTDRYALRNI
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RYTCHVQHEGLFQPLILRWEQSPQPTIPIVGIVAGIVYLGAVVTGAVVAAVWMRKKSS
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Tissue Transplantation and Immunology, Jinan University, Shipai, Guangzhou; Guangdong 510632, China
Location/Qualifiers
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                                                                                                                                                                                                                                 cell_type="peripheral leukocytes"
/dev_stage="adult"
i. .1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'product="MHC class Ib antigen"
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                                                                                               1. .1041
/organism="Homo sapiens"
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/db_xref="GI:29650891"
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/db_xref="taxon:9606"
/chromosome="6"
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/replace="g"
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                                                                                               481 GCTCAGATCACCCAGCGCTTCTATGAGGCAGAGGAATATGCAGAGGAGTTCAGGACCTAC 540
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He,X., Xu,L., Liu,Y. and Zeng,Y. Identification of a novel HiA-F allele - HLA-F*010102
Tissue Antigens 63 (2), 181-183 (2004)
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He,X., Liu,Y., Xu,L. and Zeng,Y.
Cloning of full-length HLA-F*0101 variant 1 cDNA from Han Chinese
Unpublished
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AQQYORYFBAEBRYYLGBCLELLBRYLEGHGKETLORADPYAHHAHHISDH
EATLRCWALGFYPETLTLYNGRDGEEQTQFTELVERREAGNGTFORWAAVVYPSGEEG
RYTCHVQHEGLPQPLILRWEGSPQPTIFINGINGLYGAVVTGAVVTGAVVAAVMWRKKSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.nisc.nih.gov/
Contact: nisc_mgcachgari.nih.gov/
Contact: nisc_mgcachgari.nih.gov
Akhter.N., Ayole,K., Beckstrome.Sternberg,S.M., Benjamin.B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blattich,N.L., Granite,S., Gudan,X., Gudan,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
McDowall,C., Vogt,J.L., Walker,M.A., Thomas,P.J., Touchman,J.W.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 135 Row: o Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9665231. Location/Qualifiers
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/gene="HLA-F"
/note="HG; Region: Immunoglobulin domain constant region
subfamily"
/db_xref="CDD:cd00098"
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//gene="HLA-F"
//note="HHZ-F"
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domains alpha 1 and 2"
domains alpha 1 and 2"
                                                            Direct Submission
Submitted (01-DEC-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                          WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: capbs-r@mail.nih.gov
Final: capbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
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/db_xref="taxon:9606"
/clone="MGC:74962 IMAGE:5496696"
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/db_xref="GI:38649063"
/db_xref="LocusID:3134"
/db_xref="MIM:143110"
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(bases 1 to 1167)
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1. (bases l.co.167)

S. Stausberg, R.L., Faingold, E.A., Grouse, L.H., Derge, J.G.,
Klauener, R.D., Collins, F.S., Wagner, L., Shemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.P., Jordan, H., Mozre, T., Max, S.I., Wang, J., Hsieh, P.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Parange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., Loquellano, N.A., Peters, G.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, C., Rade, S., Garcia, M., Gay, L.J., Hulyk, S.M.,
Villalon, D.K., Muzny, D.M., Godergren, E.J., Lu, X., Gibbs R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Miting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, X.S., Krzywinski, M. I., Skalska, U., Smailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAGCTGTGGTCGCTGCTGTGATGTGGAGGAAGAGAGCTCAGATAGAAACAGAGGAGC 1020
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Homo sapiens major histocompatibility complex, class I, F, mRNA (cDNA clone MGC:74962 IMAGE:5496696), complete cds.
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                              541 CTGGAGGCGAGTGCCTGGAGTTGCTCCGCAGATACTTGGAGAATGGGAAAGGAGACGCTA
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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1021 TACTCTCAGGCTGCAGT 1037
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                                                                                                                                 5 ATGGCGCCCCGAAGCCTCCTCCTCCTCTCAGGGGCCCTGGCCCTGACCGATACTTGG 64
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                                                            Gaps
                                                          0,
                 90.5%; Score 986; DB 9; Length 1167; 99.9%; Pred. No. 0; tive 0; Mismatches 1; Indels 0
                                                            Matches 1036; Conservative
                                          Best Local Similarity
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L LUSSES. L. C. D. 12.2.)

Strausberg. R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Sharmen, C.M., Schuler, G.D.,
Altechul, S.R., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Bonder, T., Wars, S.I., Wang, J., Hsielt, F.,
Diatchenko, L., Martsina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.B., Brownstein, M.J., Undian, T. B., Grantin, E., Toshiyuki, S.,
Carninci, P., Farnge, C.C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McBwan, P.J.,
Worley, K.J., Malek, J.A., Gunarane, P.H., Richards, S.,
Worley, K.J., Malek, J.A., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Schwitz, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Butterfield, X.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Orne, E. More than 15,000 full-length
                                                                                                                                                                  1523 bp mRNA linear PRI 11-DEC-2003 How sapiens major histocompatibility complex, class I, F, mRNA (CDNA close IMAGE:4039990), partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be found
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9665231.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1523)
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Submitted (08-JUN-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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On Dec 9, 2003 this sequence version replaced gi:14349361.
Contact: MGC help desk
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CDNA Library Arrayed by: The I.M A.G.E. Consortium (LINL)
DNA Sequencing by: Institute for Systems Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human and mouse cDNA sequences
Proc. Warl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman,
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Iissue Procurement: DCTD/DTP/Gazdar
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/organism="Homo sapiens"
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1025 TACTCTCAGGCTGCAGT 1041
                                                                                                                                                                                                                                                                                                                                                                         BC009260.2 GI:39644655
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dart. Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Rakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Ohayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Bositi, T., Kawi, Y., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikwa, E., Omura, Y., Abe, K., Kamihara, K., Kateuta, N., Sato, K., Tanikwa, M., Yamashita, H., Minomiya, K., Takiguchi, S., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Chiba, Y., Ishida, S., Ono, Y., Takahashi-Pujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Oshima, A., Saxo, S., Wati, Imose, N., Museshino, K., Yatana, T., Shiohata, N., Saro, S., Wati, Matsunawa, H., Satoh, N., Takami, S., Satoh, M., Sato, S., Wati, Matsunawa, H., Satoh, N., Watanabe, T., Sugiyama, A., Takama, S., Kukakami, B., Yamazaki, M., Watanabe, X., Kumagai, A., Takemoto, M., Kukakami, B., Yamazaki, M., Watanabe, X., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M.,
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Mammalia, Eutheria, Primates, Catarthini, Hominidae, Homo.
                                                                                                                           657 CAGCGCGCAGAICCTCCAAAGGCACACGTIGCCCACCCACCCCATCTCTGACCATGAGGCC
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                                                                                                     /note="synonyms: HLA-CDA12, HLAF, HLA-5.4"

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He,X., Xu,L., Liu,Y. and Zeng,Y.
Direct Submission
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Direct Submission

Direct Submission

Direct Submission

Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

Karusa-Kamatari, Kisarazu, Chiba 198-52-3978, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Research Association for Biotechnology (RAB); supported by Japan

Keysarch, Association for Biotechnology (RAB); supported by Japan

Key Technology Center Encitoned Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and Mass full insert sequencing: HRI and

RAB; annotation HRI and Mass full insert sequencing: HRI and
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Tanai, H., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Watanabe, M.,
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Wagatsuma, M., Takahashi-Pujii, A., Oshima, A., Sugiyama, A.,
and Isogai, T.,
NEDO human cDNA sequencing project
Unpublished
Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmoni, Y., Kawabata, A., Hikili, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Inch, T., Shigeta, K., Senba, T., Matsumara, K., Nakalima, Y., Mizumo, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakase, T., Nomura, K., Nakase, T., Nomura, N., Kikuchi, H., Masubo, Y., Yamashita, R., Nakai, K., Yada, T., Nakawa, Y., Obara, O., Isogai, T. and Sugano, S. Complète sequencing and characterization of 21,243 full-length
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gai, T. and Yamamoto, J.
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Submitted (10-JMN-2003) Key Laboratory of Ministry of Education for Tissue Transplantation and Immunology, Jinan University, Shipai, Guangzhou, Guangdong 510632, China Location/Qualifiers

| Jorganism="Homo sapiens" | Jorganism="Homo sap
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                               Eukaryoca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 972)
                                                                                                                                                                                                                                                                                                                                                    391 GGCTGCGACATGGGGCCCGACGGACGCCTCCTCCGCGGGTATCACCACGCGCGTACGAC
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361 GGCTGCGACATGGGGCCCCGACGCCTCCTCCGCGGGTATCACCAGCACGCGTACGAC
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903 891 963

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Liu,Y., Xu,L., Zeng,Y. and He,X.
Direct Submission
Direct Submission
Submitted (20-74N-2003) Key Laboratory of Ministry of Education for Tissue Transplantation and Immunology, Jinan University, Shipai, Guangzhou, Guangdong 510632, China
Location/Qualifiers
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Homo sapiens MHC class I antigen (HLA-F) mRNA, partial cds.
AY221102
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RCWALGFYPABITLTWQRDGEEQTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTC
HVQHEGLPQPLILRWEQSPQPTIPIVGIVAGLVVLGAVVTGAVVAAVM"
                                                                                                                                                                                              61 TCCTTGAGGTATTTCAGCACCGCTGTGTCGCGGCCCGGCCGCGGGGAGCCCCGCTACATC 120
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1. (bases 1 to 972)

Liu,Y., Xu,L., Zeng,Y. and He,X.

A new polymorphism in non-classical MHC class I HLA-F

Unpublished
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        844 GTGCAGCACGAGGGCTGCCCCAGCCCCTCATCCTGAGATGGGAGCAGTCTCCCCAGCCC
                                                    904 ACCATCCCCATCGTGGGCATCGTTGCTGGCCTTGTTGTTGGAGCTGTGGTCACTGGA
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/replace="c"
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/organism="Homo sapiens"
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 822)
Egawa, K.

PAT 17-JUL-2003

linear

DNA

822 bp Di Cancer prophylactic/treatment agent. BD187422

DEFINITION ACCESSION VERSION

BD187422 LOCUS RESULT 13

BD187422.1 GI:32997161 JP 2003012544-A/2. Homo sapiens (human) Homo sapiens

SOURCE ORGANISM

KEYWORDS

REFERENCE AUTHORS

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linear PAT 27-NOV-2002
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                       664 CTGAGGTGCTGGGCCCTGGGCTTCTACCCTGCGGAGATCACGCTGACCTGGCAGCGGGAT 723
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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0; Gaps
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/db_xref="taxon:9606"
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Sequence 2 from Patent BP1245675.
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G01N33/53,G01N33/574,G01N33/68//(C12N1/21,C12R1:19),(C12P21/02, PC
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Mammaliai Eutheria; Primates; Catarrhini; Hominidae; Homo.
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75.5%; Score 822; DB 6; Length 822;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 822; Conservative 0; Mismatches 0; Indels
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Patent: JP 2001095584-A 2 10-APR-2001;
Patent: JP 2001095584-A 2 10-APR-2001;
SJ Homo sapiens (human)
PN JP 2001095584-A/2
PP 10-APR-2001
PF 30-SEP-1999 JP 1999279566
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E63814.1 GI:22553652
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Homo sapiens (human)
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aah45555 Human can	Adf55584 DNA encod	Adj74945 Marker ge	Marker	Adp10447 Reference	Aas90913 DNA encod	Aas90740 DNA encod	Adi21449 Novel hum	Aah45556 Human can	Adf55585 DNA encod	Aac78195 Human can	Aah45557 Human can	Adf55586 DNA encod	Aac00215 Human sec	Ach50642 Human mam	Abx74535 Human cDN	Adi21922 Novel hum	Aba83122 HLA-Cw ov	Abn97218 Gene #371	Adb53954 HLA-F gen	Aak86871 Human imm
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10	AAH45555	ADF55584	ADJ74945	ADJ74851	ADP10447	AAS90913	AAS90740	ADI21449	AAH45556	ADF55585	AAC78195	AAH45557	ADF55586	AAC00215	ACH50642	ABX74535	ADI21922	ABA83122	ABN97218	ADB53954	AAK86871
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% Query Match	100.00	100.0	100.0	100.0	100.0	87.4	87.4	87.4	75.5	75.5	72.2	59.2	59.2	33.1	32.6	31.1	26.5	25.6	25.6	25.6	25.4
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ALIGNMENTS

This invention relates to a cancer cell specific HLA-F antigen. The invention includes DNA encoding the antigen, and a method for the preparation of the cancer cell specific HLA-F antigen. The antigen may be used in a method to diagnose cancer, in which the protein is used to detect anti-HLA-F antibodies in bodily fluids of the patient. The present sequence represents DNA encoding the cancer cell-specific HLA-F antigen Novel cancer cell-specific HLA-F antigen useful for diagnosing cancer. Human cancer cell specific HLA-F antigen encoding DNA SEQ ID 1. Location/Qualifiers
1.1089
1.1084
/product= "Cancer cell specific HLA-F antigen" HLA-F antigen; cancer cell specific; human; ds. Claim 3; Page 8-9; 12pp; Japanese. AAH45555 standard; DNA; 1089 BP. 99JP-00279566. 99JP-00279566. 12-SEP-2001 (first entry) WPI; 2001-360493/38. (EGAW/) EGAWA K. (MEDI-) MEDINET KK. (KIMU/) KIMURA K. P-PSDB; AAG64617. JP2001095584-A. 30-SEP-1999; Homo sapiens. 30-SEP-1999; 10-APR-2001. AAH45555; RESULT 1 AAH45555

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Claim 1; SEQ ID NO 1; 19pp; Japanese.
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1. .1089
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(MEDI-) MEDINET KK.
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cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL;
major histocompatibility complex; MHC; cancer cell; human; gene; ds.
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1089; Conservative 0; Mismatches 0; Indels 0;
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/product= "Cancer-cell specific HLA-F antigen"
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1081 AAAGTGTGA 1089

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121	CCCCGGTACATCGCCGTGGAGTACGTAGACACACACACAATTCCTGCGGTTCGACAGCGAC 180
181	GCCGCGATTCCGAGGATGGAGCCGCGGAGCCGTGGGTGGAGCAAGAGGGGCCGCAGTAT 240
241	TGGGAGTGGACCACAGGGTACGCCAAGGCCAACGCACAGACTGACCGAGTGGCCCTGAGG 300
301	AACCTGCTCCGCCGCTACAGCGGAGCGAGCTGGGTCTCACACCCTCCAGGGAATGAAT
361	GGCTGCGACATGGGGCCCCGACGACCTCCTCCGCGGGTATCACCACGCGCGTACGAC 420
421	GGCAAGGATTACATCTCCCTGAACGAGACCTGGGCTCCTGGACGGGGGGGG
481	GCTCAGATCACCCAGGCTTCTATGAGGCAGAGAATATGCAGAGGAGTTCAGGACCTAC 540
541	CTGGAGGGCAGTGCCTGGAGTTGGTCCGCAGATACTTGGAGAATGGGAAGGAGGCGCTA 600
601	CAGCGCGCAATCCTCCAAAGGCACACGTTGCCCACCCCATCTCTGACCATGAGGC 660
661	ACCCTGAGGTGCTGGGCCTCGGGCTTCTACCCTGCGGAGATCACGCTGACCTGGCGGGGGGGG
721	GATGGGGAGGAACACCCAGGACACACATGTGGAGACCCAGGCCTGCAGGGGATGGA 780
781	ACCTTCCAGRAGTGGGCCGCTGTGGTGGTGCCTTCTGGRGAGGAACAGAGATACACATGC 840
841	CATGTGCAGCACGAGGGCTGCCCCAGCCCCTCATCCTGAGATGGGAGCAGTCTCCCCAG 900
901	CCCACCATCCCCATCGTGGGGCATCGTTGCTGGCCTTGTTGTCCTTGGAGCTGTGGTCACT 960
961	GGAGCTGTGGTCGCTGCTGTGATGTGGAGGAGAGAGGCTCAGATAGAAACAGAGGGGAGC 1020
1021	TACTCTCAGGCTGCAGTCACTGACAGTGCCCAGGGCTCTCGGGGTGTCTCTCACAGCTAAT 1080
1081	AAAGTGTGA 1089

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bronchial asthma; chronic obstructive pulmonary disease; respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic; gene therapy; marker gene; gene; ds.
                                                                                                                                                                   Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
            ADJ74945 standard; DNA; 1188 BP.
                                                                                                                         04-AUG-2003; 2003EP-00254857.
                                                                                                                                     06-AUG-2002; 2002JP-00229312.
20-MAR-2003; 2003JP-00077212.
                                    20-MAY-2004 (first entry)
                                               Marker gene SEQ ID NO:197
                                                                                                                                                        (GENO-) GENOX RES INC.
                                                                                                                                                                                WPI; 2004-193155/19.
                                                                                                 EP1394274-A2.
                                                                                    Homo sapiens.
                                                                                                             03-MAR-2004.
                       ADJ74945;
RESULT 3
ADJ74945
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Testing for bronchial asthma or chronic obstructive pulmonary disease by comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a healthy subject.

Claim 1; SEQ ID NO 197; 241pp; English.

The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial colls are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. Also described: (l) a reagent (l) for testing for bronchial asthma or chronic obstructive pulmonary disease; (3) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma in a mouse; (5) a method for producing an animal model for bronchial asthma in a mouse; (5) a method for producing an animal model for bronchial asthma or chronic obstructive pulmonary disease; (d) a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, (e) a therapeutic agent for bronchial asthma or antisense nucleic acid corresponding to a portion of the marker gene or an antisense nucleic acid corresponding to a portion of the marker gene or an antisense nucleic acid corresponding to a portion of the marker gene or an antisense nucleic acid corresponding to a portion of the marker gene or an antisense nucleic acid corresponding to a portion of the marker gene in antisense uncleic acid corresponding to a portion of the marker gene in antisense uncleic acid corresponding to a protoin obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene. (1) has respiratory and antistimatic activities, and can be used in gene therapy. The method is u

Seguence 1188 BP; 261 A; 343 C; 375 G; 209 T; 0 U; 0 Other;

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The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of amarker gene in a biological sample from a method comprises or chronic obstructive pulmonary disease. The marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial sashma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interlevikin-13; Also described; (l) a reagent (l) for testing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent to treat bronchial asthma or chronic obstructive pulmonary disease; (s) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (s) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (s) a marker gene or an antisense nucleic acid corresponding to a portion of sthma or chronic obstructive pulmonary disease; (s) a marker gene or an antisense nucleic acid corresponding to a portion of the gene, a ribozyme, a polynucleotide that suppresses the marker gene, a ribozyme, a polynucleotide that suppresses the marker gene immobilised to assay a marker gene; and chronic obstructive pulmonary disease, on which a procein encoded by a marker gene; and (1) a marker gene; and (1) and an antisense and conservative pulmonary disease, on which a procein encoded by a marker gene; and (1) and care pulmonary disease, on which a procein encoded by a marker gene; and (1) and care pulmonary disease, on which a procein encoded by a marker gene; and (1) and care pulmonary disease, on which a non antisense and care pulmonary disease, on which a procein encoded by a marker gene; and (1) and care pulmonary disease, on which and antisethmatic activities, and can be used in gene through or screening for a therapeutic agent for procein a
1021 TACTCTCAGGCTGCAGTCACTGACAGTGCCCAGGGCTCTGGGGTGTCTCTCAGGCTAAT 1080
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20-MAR-2003; 2003JP-00077212.
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 bronchial asthma or chronic obstructive pulmonary disease. The present sequence is used in the exemplification of the present invention.
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The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in cell transplant rejection, or mechanical organ replacement rejection, in an individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases, multiple sclerosis, HIVAIDS or viral, bacterial or fungal infection. The present sequence represents a mRNA reference sequence for a 50 mer oligonucleotide marker for diagnosis and monitoring of allograft rejection and other disorders.
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                                                                                                                      TACTCTCAGGCTGCAGTCACTGACAGTGCCCAGGGCTCTGGGGGTGTCTCTCACAGCTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transplant rejection; immune system; rheumatoid arthritis; lupus; inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1089; DB 12; Length 1188; 100.0%; Pred. No. 0; Live 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prentice J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reference mRNA sequences for marker probe #124.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 80; SEQ ID NO 456; 1762pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADP10447 standard; DNA; 1188 BP
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20-DEC-2002; 2002US-00325899.
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1 ATGGCGCCCGAAGCTCCTCCTGCTGCT	61 GCGGGCTCCCACTCCTTGAGGTAITTCAG	121 CCCGGCTACATCGCCGTGGAGTACGTAGA	181 GCGGGATTCCGAGGATGGAGCGGGGA 	241 TGGGAGTGCACCACAGGGTACGCCAAGGC	301 AACCTGCTCCGCGCTACAACCAGAGGGA	361 GGCTGCGACATGGGGCCCGACGGACGCCT	421 GGCAAGGATTACATCTCCCTGAACGAGGA	481 GCTCAGATCACCCAGGCCTTCTATGAGGC	541 CIGGAGGGGAGTGCCTGGAGTTGCTCCG	601 CAGGGGGAGATCCTCCAAAGGCACAGGT	661 ACCCTGAGGTGCTGGCCCTGGGCTTCTA	721 GATGGGGAGGAACAGACCCAGGACACAGA	781 ACCITCCAGAAGTGGGCCGCTGTGGTGGTGTTGTTGTTGTTGTTGTTGTTG	841 CATGTGCAGCACGAGGGGTGCCCCAGCC	901 CCCACCATCCCATGTGGGGATCGTTGC	961 GGAGCTGTGGTCGCTGCTGTGATGTGGAG	1021 TACTCTCAGGCTGCAGTCACTGACAGTGC	1081 AAAGTGTGA 1089

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, and for chromosome and gene mapping, and in recombinant production of (II). (IT) epolymucleotides are laboused of in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in game therapy techniques to restore normal cutivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders or polypeptide and polymucleotide sequences have applications in diagnostics, formsics, gene mapping, identification of mutations in diagnostics formsics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess bliddversity and to produce other types of data and products dependent on DNA and and confine sequences. AAS64197-AAS94564 represent novel human diagnostic amino acid sequences. AAS94197-AAS94564 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGGCGCCCCGAAGCCTCCTCCTGCTCTCAGGGGCCCTGGCCCTGACCGATACTTGG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2034 BP; 545 A; 511 C; 628 G; 350 T; 0 U; 0 Other;
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tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                           DNA encoding novel human diagnostic protein #26717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 26717; 103pp; English.
                                                                                                    AAS90913 standard; cDNA; 2034 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001, 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT;
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23-AUG-2000; 2000US-00649167.
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Matches 1002, Conservative
1081 AAAGTGTGA 1089
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P-PSDB; ABG26726.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                      WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biodiversity.
                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                             AAS90913;
                                                          RESULT 6
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain recardion (PCR) primers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cutivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating a useful for generating antibodies against it, detecting or quantitating of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in diagnostics for genefic disorders or other trails to assess bliddiversity responsible for genefic disorders or other trails to assess bliddiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences. AAS64197-AAS94564 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the invented specification, but was obtained in the wing and produces and the printed sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    991 GCGGGCTCCCACTCCTTGAGGTATTTCAGCACCGCTGTGTCGCGGCCCGGGCCGGGGGAG 1050
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                                       Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87.4%; Score 952; DB 5; Length 2037; 99.9%; Pred. No. 0; ive 0; Mismatches 1; Indels C
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DNA encoding novel human diagnostic protein #26544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 26544; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                               Tang YT;
                                                                                                                                                                                                                     30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                             31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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Best Local Similarity 99.99
Matches 1002, Conservative
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P-PSDB; ABG26553.
                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                       WO200175067-A2
                                                                                                    Homo sapiens.
                                                                                                                                                                              11-OCT-2001.
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                   988 GCGGGCTCCCACTCCTTGAGGTATTTCAGCACCGCTGTGTCGCGGCCCCGGCGCGGGGAG 1047
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                                                                                                                 1048 CCCCGCTACATCGCCGTGGAGTACGTAGACGACACGCAATTCCTGCGGTTCGACAGGGAC 1107
                                                                                                                                                                                                  TGGGAGTGGACCACAGGGTACGCCAAGGCCAACGCACAGACTGACCGAGTGGCCCTGAGG 1227
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                                                                              CCCCGCTACATCGCCGTGGAGTACGTAGACGACGCAATTCCTGCGGTTCGACAGCGAC 180
                                                                                                                                                        GCCGCGATTCCGAGGATGGAGCCGCGGGAGCCGTGGGAGCAAGAGGGGGCCCCCAGTAT 240
                                                                                                                                                                                                                                         TGGGAGTGGACCACAGGGTACGCCAAGGCCAACGCACAGACTGACCGAGTGGCCCTGAGG 300
                                                                                                                                                                                                                                                                                                                        GGCAAGGATTACATCTCCCTGAACGAGCTGCGCTCCTGGACCGCGGGGGGACACACCGTG 480
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(first entry)

13-FEB-2002

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The invention relates to an isolated polynucleotide encoding a polypeptide with biological activity. The polynucleotides and polypeptides are useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in come cartiage, tendon, ligament and/or nerve tissue growth or regeneration, in wound healing, in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents a novel human expressed sequence tag, EST.
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Drmanac RT,
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Ghosh M,
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(MEDI-) MEDINET KK.
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This invention relates to a cancer cell specific HLA-F antigen. The invention includes DNA encoding the antigen, and a method for the preparation of the cancer cell specific HLA-F antigen. The antigen may be used in a method to diagnose cancer, in which the protein is used to sequence arti-HLA-F antibodies in bodily fluids of the patient. The present sequence represents DNA encoding the cancer cell-specific HLA-F antigen of the invention
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721 TICCAGAAGIGGGCCGCIGIGGIGGCGTICCIGGAGGAACAGAGAIACACAIGCCAI 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "This seguence lacks both start and stop codons"
                                                                                                                                                                                                                                                                                                                                                                                DNA encoding fragment #1 of human cancer-cell specific HLA-F antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agent for preventing and treating cancer, comprising human leukocyte antigen-F DNA, or a plasmid or viral vector comprising the DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Cancer; human leukocyte antigen-F; HLA-F; cancer-cell specific HLA-F antigen; cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; cancer cell; human; gene;
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                                                                                                                                                                                                                               ADF55585 standard; DNA; 822 BP
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(MEDI-) MEDINET KK.
(KIMU/) KIMURA Y.
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61 GGCTACATCGCCGTGGAGTACGTAGACGACACGCAATTCCTGCGGTTCGACAGCGGACGCC 120
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                                                                                                                                                                                                     481 GCTCAGATCACCCAGCGCTTCTATGAGGCAGAGGAATATGCAGAGGAGTTCAGGACCTAC
                                                                                                                                                                                                                                      500 GCTCAGATCACCCAGCGCTTCTATGAGGCAGAGGAATATGCAGAGGAGTATCAGGACTTCAGGACCTAC
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                                                                                                             421 GGCAAGGATTACATCTCCCTGAACGAGCACCTGCGCTCCTGGACCGCGGGGGGACACCGTG
                                                                                                                                                                                                                                                                                                     CTGGAGGGCGAGTGCCTGGAGTTGCTCCGCAGATACTTGGAGAATGGGAAAGGAGACGCTA
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P-PSDB; AAG64619.
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(MEDI-) MEDINET KK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB4239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary, immunomodulator; antidiabetic; antiathmatic; antitherary; immunomodulator; antidiabetic; antibated; antitherary; immunomodulator; antidiabetic; antiportacid; antitherary; immunomodulator; cantiniformantory; antiportacid; antitherary; immunomodulator; antidiabetic; antiportacid; antiportacid; antiportacid; antiportacid; antiportacid; antiportacid; antiportacid; and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thromolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and antagonists may be also be used in drug screens. AAC78451 of AAC78457 and AAB44240 represent sequences used in the exemplification of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 1111-1112; 2352pp; English.
                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                      38-MAR-2000; 2000WO-US005882
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P-PSDB; ADF55589.
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(MEDI-) MEDINET KK.
(KIMU/) KIMURA Y.
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    Homo sapiens.
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This invention relates to a cancer cell specific HLA-F antigen. The invention includes DNA encoding the antigen, and a method for the preparation of the cancer cell specific HLA-F antigen. The antigen may be used in a method to disgnose cancer, in which the protein is used to detect anti-HLA-F antibodies in bodily fluids of the patient. The present sequence represents DNA encoding the cancer cell-specific HLA-F antigen
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                                                                                                                              Score 645; DB 4; Length 645;
Pred. No. 9e-296;
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                                                                                                        Sequence 645 BP; 143 A; 194 C; 215 G; 93 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 ATCGCCGTGGAGTACGTAGACGACACGCAATTCCTGCGGTTCGACAGCGACGCCGCGGGATT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                    /note= "This sequence lacks both start and stop codons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATCGCCGTGGAGTACGTAGACGACGCAATTCCTGCGGTTCGACACGCGCGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 CCGAGGATGGAGCCGCGCGCAGCCGTGGGTGGAGCAAGAGGGGCCGCAGTATTGGGAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 accacadedraceccaageccaacecaceaceaceaceaceaceaceccreaeeaacerecre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agent for preventing and treating cancer, comprising human leukocyte antigen-F DNA, or a plasmid or viral vector comprising the DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 59.2%; Score 645; DB 10; Length 6
Best Local Similarity 100.0%; Pred. No. 9e-296;
Matches 645; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 3; 19pp; Japanese.
Location/Qualifiers
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The present sequence is one of a large number of 5' ESTs derived from manks encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length gene therapy and chromosome mapping procedures. They are used to obtain full segment therapy and chromosome mapping procedures. They are used to obtain upper contain regulatory sequences and to design expression and secretion
GATCCTCCAAAGGCACACGTTGCCCACCACCCCATCTCTGACCATGAGGCCACCTGAGG 669
                                                                                                                                                                                                                                                                                                                   GATCCTCCAAAGGCACACGTTGCCCACCCCCATCTCTGACCATGAGGCCACCCTGAGG 540
                                                                                                                                                                                                                                                                                                                                                                                                TGCTGGGCCCTGGGGCTTCTACCCTGCGGAGATCACGCTGACCTGGCAGGGGGATGGGGAG 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                            GAGTGCCTGGAGTTGCTCCGCAGATACTTGGAGAATGGGAAGGAGGACGCTACAGCGCGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   601 GAACAGACCCAGGACACAGAGCTTGTGGAGACCAGGCCTGCAGGG 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 424 BP; 79 A; 137 C; 139 G; 69 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAACAGACCCAGGACACAGAGCTTGTGGAGACCAGGCCTGCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein 5' EST, SEQ ID NO: 213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC00215 standard; cDNA; 424 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-FEB-2000; 2000EP-00200610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WFI; 2000-500381/45.
P-PSDB; AAG00209.
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33.1%; Score 361; DB 3; Length 424;

Query Match

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                                                                                                               124 GCGGGCTCCCACTCCTTGAGGTATTTCAGCACCGCTGTGTGTCGCGGCCCCGGCCGCGGGGGAG 183
                                                                                                                                      CCCCGCTACATCGCCGTGGAGTACGTAGACGACACGCAATTCCTGCGGTTCGACAGCGAC 180
                                                                                                                                                               243
                                                                                                                                                                                                                303
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                                                                                                                                                                                                                                                         Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polymucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antiesnse DNA or RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated polynucleotide comprising any one of
                                       9
                                                      64 ATGGCGCCCCGAAGCCTCCTCCTGCTCTCAGGGGCCCTGGCCCTGACCGATACTTGG
                                                                                      GCGGGCTCCCACTCCTTGAGGTATTTCAGCACCGCTGTGTGTCGCGGCCCGGCCGCGGGGAG
                                                                                                                                                              coccectacatoscorseasatacerasaceaceceaatrocosestrosacases
                                                                                                                                                                                        244 GCCGCGATTCCGAGGATGGAGCCGCGCGGCGTGGGTGGAGCAAGAGGGGCCGCAGTAT
                                                                                                                                                                                                                                         TGGGAGTGGACCACAGGGTACGCCAAGGCCAACGCACAGACTGACCGAGTGGCCCTGAGG
                                     1 ATGGCGCCCCGGAAGCCTCCTCCTGCTGCTCTCAGGGGCCCTGGCCCTGACCGATACTTGG
              0; Gaps
              0; Indels
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  Pred. No. 6.3e-161;
            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stache-Crain B,
                                                                                                                                                                                                                                                                                                                                                                                                                              ACH50642 standard; cDNA; 487 BP.
  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human mammary gland cDNA #47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-OCT-2003 (first entry)
Best Local Similarity 100. Matches 361; Conservative
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STACHE-CRAIN B.
DICKSON M C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT, Labat I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DRMANAC R T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-615964/58.
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determined by the technique of SBH (sequencing by hybridisation). Also determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novlp polymucleotide. The nucleic acid sequences are adong frame of the novlp polymucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (SST) for identifying expressed genes or for physical mapping of the human genome, in forenside, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for FCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA or RNA. The purified polypeptide is one of the 38043 isolated cDNA/SST sequences. Note: The sequence data obtained in electronic format directly from USPTO at sequence data obtained in electronic format directly from USPTO at sequence than sequence contains an electronic format directly from USPTO at sequence than sequence contains and sequence 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 GCGGGAGCCGTGGGTGGAGCAAGAGGGCCGCAGTATTGGGAGTGGACCACAGGGTACGC 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 GAGCGAGGCTGGGTCTCACACCCTCCAGGGAATGAATGGCTGCGACATGGGGCCCCGACGG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 GCGGGAGCCGTGGGTGGAGCAAGAGGGCCGCAGTATTGGGAGTGGACCACACGGGTACGC 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 32.6%; Score 355; DB 9; Length 487;
Best Local Similarity 100.0%; Pred. No. 4.4e-158;
Matches 355; Conservative 0; Mismatches 0; Indels 0; Gaps
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Search completed: December 16, 2004, 13:07:23 Job time : 637 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 213, App
Sequence 322, App
Sequence 130, App
                                                                                                                                  December 16, 2004, 12:56:48; Search time 120 Seconds (without alignments) 6450.409 Million cell updates/sec
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1 atggcgccccgaagcctcct......tcacagctaataaagtgtga 1089
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Sequence
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Sequence 4
Sequence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lssued_Patents_NA:*
1: /cgT2_6/ptodata1/ina/5A_COMB.seq:*
2: /cgT2_6/ptodata1/ina/5B_COMB.seq:*
3: /cgT2_6/ptodata1/ina/6A_COMB.seq:*
4: /cgT2_6/ptodata1/ina/6B_COMB.seq:*
5: /cgT2_6/ptodata1/ina/FUTUS_COMB.seq:*
6: /cgT2_6/ptodata1/ina/PacFUTS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                               824507 seqs, 355394441 residues
                                                                                             OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                      OLIGO_NUC
Gapop_60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length
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Perfect score:
Sequence:
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EC
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Sequence 11566, A sequence 2, Appli Sequence 6, Appli Sequence 6, Appli Sequence 35, Appl Sequence 325, Appl
                                                                                                                                                                                                                                    Sequence 323, App
Sequence 1114, Ap
Sequence 1, Appli
Sequence 3, Appli
Sequence 35, Appli
Sequence 1087, Ap
Sequence 1087, Ap
Sequence 1087, Ap
Sequence 1087, Ap
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US-09-513-999C-213

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#ESULA.

#ERICANT: Dumas Milne Edwards, J.B.

#PPLICANT: Duclart, A.

#PPLICANT: Duclart, A.

#PLICANT: Giordano, J.Y.

#ITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

#PLICANT: PLICANT: Giordano, J.Y.

#ITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

#PLICANT: PRICANT: US-082.

##ERICANT FILING DATE: 2000-02-24

##ERICANT FILING DATE: 1999-02-26

##ERICANT: NUMBER: US 60/122,487

##ERICANT: PRICANT: 1999-02-26

##ERICANT: US-26

##ERICANT: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCCGCTACATCGCCGTGGAGTACGTAGACGACACGCAATTCCTGCGGTTCGACAGCGAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303
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US-08-577-081A-40

US-08-914-372C-2

US-08-914-372C-4

US-08-914-372C-4

US-08-914-372C-4

US-08-914-372C-3

US-09-799-451-323

US-09-799-451-323

US-09-799-451-323

US-09-743-172C-3

US-08-914-372C-3

US-08-914-372C-3

US-08-914-372C-3

US-08-914-372C-3

US-08-914-372C-3

US-09-705-1087

US-09-705-1087

US-09-705-1087

US-09-614-1325-1087

US-09-614-1325-1087
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NAME/KEY: sig_peptide
LOCATION: 64.114
OTHER INFORMATION: score 9.3
OTHER INFORMATION: seq_SLLLLSGALALT/DT
          TYPE: DNA ORGANISM: Homo sapiens
          ; US-09-513-999C-213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
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              61
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TYPE: DNA
                                                                                                                    364 AACCIGCICCGCCGCTACAACCAGAGCGAGGCTGGGTCTCACACCCCCCCAGGGAAIGAAI 423
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241 TGGGAGTGGACCACGGTACGCCAAGGCCAACGCACAGACTGACGGAGTGGCCCTGAGG 300
                                         304 TGGGAGTGGACCACAGGGTACGCCAAGGCCAACGCACAGACTGACCGAGTGGCCCTGAGG 363
                                                                                    632 CCCACCACCCCATCTCTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGCTTCTACC 691
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100.0%; Pred. No. 5.4e-25;
tive 0; Mismatches 0; Indels 0
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TITLE OF INVENTION: No. 6783869e1 Nucleic Acids and
TITLE OF INVENTION: No. 6783869e1 Nucleic Acids and
TITLE OF INVENTION: No. 6783869e1 Nucleic Acids and
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: Dt. FL. genes Version 2.0
LENGTH: 1221
                                                                                                                                                                                                                                                                                                                               Sequence 322, Application US/09799451
Patent No. 6783969
GENERAL INFORMATION:
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Sequence 130, Application US/09566921
Patent No. 6682888
GENERAL INFORMATION:
APPLICANT: Lorling, Jeanne F.
APPLICANT: Tingley, Debora W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhao, Qing A.
Wang, Jian-ui
Ma, Yunging
Yamazaki, Victoria
Chen, Rui-hong
Wang, Zhiwei
Wang, Zhiwei
Wang, Dunrui
Yang, Yonghong
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Best Local Similarity 100.0
Matches 73; Conservative
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APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Aeundi, Vinod
APPLICANT: Ren, Feiyan
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Xue, Aidong J.
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Ghosh, Reena
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ORGANISM: Homo sapiens
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; LOCATION: (1)..(213)
US-09-799-451-322
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US-09-799-451-322
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632 CCCACCACCCCATCTCTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGGCTTTCTACC 691
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6.7%; Score 73; DB 4; Length 1559;
Best Local Similarity 100.0%; Pred. No. 5.3e-25;
Matches 73; Conservative 0; Mismatches 0; Indels
APPLICANT: Edwards, Carla M.
TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
TILE REFERENCE: PA-0024 US
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ghosh, Reena APPLICANT: Ghosh, Reena TITLE OF INVENTION: No. 678396991 Nucleic Acids and TITLE OF INVENTION: No. 678396991 Nucleic Acids and TITLE OF INVENTION: Polypeptides FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILLS DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: DE-FL-genes Version 2.0
SEQ ID NO 31-15-9
                                                                                                                                                                                                                                                                                        NAMB/KEY: misc feature
) OTHER INFORMATION: Incyte ID No. 6682888 1040429.6
US-09-566-921-130
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Patent No. 6783969
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Yamazaki, Victoria
Chen, Rui-hong
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APPLICANT: Zhou, Phng
APPLICANT: Goodrich, Ryle
APPLICANT: Ren, Fażyan
APPLICANT: Ren, Fażyan
APPLICANT: Zhang, Jie
APPLICANT: Xue, Aidong J.
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Yang, Yonghong
Wehrman, Tom
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Wang, Jian-Rui
                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhiwei
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US-09-799-451-317
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US-09-799-451-317
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LENGTH: 1521
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632 CCCACCACCCATCTCTGACCATGAGGCCACCTGAGGTGCTGGGCCCTGGGCTTCTACC 691

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.0%; Score 65; DB 4; Length 152; Best Local Similarity 100.0%; Pred. No. 3.6e-21; Matches 65; Conservative 0; Mismatches 0; Indels
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TITLE OF INVENTION: No. 6783969el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBERS
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
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CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: PL_Genes Version 2.0
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Yamazaki, Victoria
Chen, Rui-hong
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APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
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Wang, Jian-Rui
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; LOCATION: (1140)..(1769)
US-09-799-451-318
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Ren, Feiyan
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                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-12022
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                                                                                                                                                                                                                                                                SEQ ID NO 12022
LENGTH: 152
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APPLICANT:
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APPLICANT: TYAN, DOLLY B.

TITLE OF INVENTION: METHOD FOR DETERMINING GENETIC

TITLE OF INVENTION: PRESISPOSITION FOR SERONEGATIVE SPONDYLOARTHROPATHIES AND

TITLE OF INVENTION: PRODUCTS THEREFOR

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 4365 Executive Drive, Suite 1500

CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2269 CCCACCACCCCATCTCTGACCATGAGGCCACCCTGAGGTGCTGGGCCTGGGCTTCTACC 2328
685 CCCACCACCCATCTCTGACCATGAGGCCACCTGAGGTGCTGGGCCTTGGGCTTTACC 744
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Patent No. 6783961
Patent No. 6783961
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 6.7%; Score 73; DB 1; Length 6553; Local Similarity 100.0%; Pred. No. 5e-25; les 73; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
REPLICATION NUMBER: US/08/522,942
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08522942
Patent No. 5753442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 37,915
REPERBURG/DOCKET NUMBER: P07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-1995
TELEPAX: 619-546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ramos, Robert T.
REGISTRATION NUMBER: 37,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2329 crecesadarcae 2341
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STRANDEDNESS: both
TOPOLOGY: both
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0
                                                                                                                                                Query Match
4.8%; Score 52; DB 4; Length 2225;
Best Local Similarity 100.0%; Pred. No. 4.6e-15;
Matches 52; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 4.5e-15;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08564313
Patent No. 5910488
GENERAL INFORMATION
APPLICANT: Nabel, Gary
APPLICANT: Lew, Denise
APPLICANT: Marquet, Magda
TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Knobbe, Martenë, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VICAL.033CP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,313
FILING DATE: 01-DEC-1995
CLASSIPRICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/074,344
FILING DATE: 07-UN-1993
ATTORNEY AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: VI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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Best Local Similarity 100.0
Matches 52; Conservative
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1140)..(1769)
US-09-799-451-318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 619-235-85: TELEFAX: 619-235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
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CLONE: HLA-B7
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COUNTRY: USI
ZIP: 92660
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                                                                                                                                              Sequence 84, Application US/09220132
Sequence 84, Application US/09220132
Patent No. 6506607
GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: METHODS AND COMPOSITONS FOR THE IDENTIFICATION AND ASSESSMENT
FILE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCE
FILE REPERRINCE: 07334-074001
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/079,303
PRIOR APPLICATION NUMBER: US 60/069,821
PRIOR PILING DATE: 1999-03-25
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 191
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1690 TCTCTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGGCTTCTACCCTGCGGAGATCA 1749
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TITLE OF INVENTION: No. 6783969el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SEQ ID NO 319
LENGTH: 2225
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Patent No. 6783969
GENERAL INFORMATION:
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Yamazaki, Victoria
Chen, Rui-hong
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GENERAL INFORMATION.
APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
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Yang, Yonghong
Wehrman, Tom
Ghosh, Reena
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Wang, Jian-Rui
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
CORGANISM: Homo sapiens
US-09-220-132-84
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US-09-799-451-318
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LENGTH: 3520
                                                                                                           RESULT 8
US-09-220-132-84
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APPLICANT:
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APPLICANT:
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ZIP: 92660
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2243 CCACCACCCCTCTCTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGG 2192
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                                                                                                                                                                  APPLICANT: Regente of the University of Michigan APPLICANT: Regente of the University of Michigan APPLICANT: Nabel, Elizabeth APPLICANT: Nabel, Elizabeth APPLICANT: Nabel, Gary APPLICANT: Lew, Denise APPLICANT: Marquet, Magda TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY NUMBER OF SEQUENCES: 2 CORRESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: ADDRESSE: Knobbe, Martens, Olson and Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 4.8%; Score 52; DB 5; Length 4059; 1. Similarity 100.0%; Pred. No. 4.5e-15; 52; Conservative 0; Mismatches 0; Indels
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RR: VICAL.033VPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP. 22660
COMPUTER REAABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.1
CURRENT APPLICATION NAMBER: PCT/US94/06069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRICATION:
PRICA APPLICATION DATA:
APPLICATION NUMBER:
08/074,344
FILING DATE: 07-JUN-1993
ATTORNEY/AGRENT INFORMATION:
NAME: 1eraeleen, Ned
REGISTRATION NUMBER: 29,655
TELECOMMUNICATION:
TELEPHONE: (419-235-856)
                                                                                                                                  Sequence 2, Application PC/TUS9406069 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-564-313-1

Sequence 1, Application US/08564313

Patent No. 5910488

GENERAL INFORMATION:

APPLICANT: Nabel, Blizabeth

APPLICANT: Nabel, Gary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 4059 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 619-235-0176
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: circu
MOLECULE TYPE: CI
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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FRAGMENT TYPE:
                                                                                         RESULT 11
PCT-US94-06069-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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632 CCCACCACCCCATCTCTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGG 683
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4.8%; Score 52; DB 2; Length 4965;
Best Local Similarity 100.0%; Pred. No. 4.5e-15;
Matches 52; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
PCT-US94-06069-1
| Sequence 1, Application PC/TUS9406069
| Sequence 1, Application PC/TUS9406069
| APPLICANT: Nacl Incorporated | APPLICANT: Regents of the University of Michigan APPLICANT: Nabel, Elazabeth APPLICANT: Nabel, Gary | APPLICANT: Nabel, Gary | APPLICANT: Nabel, Gary | APPLICANT: Navouet, Magda | TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY | TOTALE OF SEQUENCES: | ADDRESSEE: Knobbe, Martens, Olson and Bear | STREET 620 Newport Center Drive 16th Floor | CITY: Newport Beach | STATET CAD
APPLICANT: Lew, Denise
APPLICANT: Marquet, Magda
TITLE OF INVENTION: PLASMIDS SUITABLE FOR GENE THERAPY
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                SSEE: Knobbe, Martens, Olson and Bear
1: 620 Newport Center Drive 16th Floor
Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VICAL.033CP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
GOFRANDG SYSTEM: DOS
GORDATING SYSTEM: DOS
GORDATING SYSTEM: DOS
GORDATING SYSTEM: DOS
GORDATION DATA:
APPLICATION NUMBER: U$/08/564,313
FILING DATE: 01-DEC-1995
CLASSIERCATION: 514
PRIOR APPLICATION NUMBER: U$/074,344
FILING DATE: 07-UN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: VICAL.033CP
TELECHONICATION INFORMATION:
TELECHOMINICATION INFORMATION:
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FRAGMENT TYPE:
INMEDIATE SOURCE:
CLONE: HLA-B7 and Beta-2
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SEQUENCE CHARACTERISTICS:
LENGTH: 4965 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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STREET: 62
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Query Match
Best Local Similarity 100.0
Matches 50; Conservative
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US-09-397-787-329
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US-09-397-787-329
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; LOCATION:
US-08-403-853-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 4.8%; Score 52; DB 5; Length 4965; Best Local Similarity 100.0%; Pred. No. 4.5e-15; Matches 52; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE: US/08/403,853
FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: KORRY, Alex A.
APPLICANT: IRVING, Robert A.
APPLICANT: IRVING, Robert A.
APPLICANT: ATWELL, John L.
APPLICANT: PALBY, Robyn L.
APPLICANT: COMER, Barbara E.
APPLICANT: COLMAN, PETER M.
APPLICANT: COLMAN, PETER M.
APPLICANT: COLMAN, PATGET BINDING POLYPEPTIDE NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                     VICAL.033VPC
                  MEDIUM TYPE: Diskette
COMPUTER: IBM COMMASTIDIE
COMPUTER: IBM COMMASTEN
SOFTWARE: FASTERN 'OSS
SOFTWARE: FASTERN VATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06069
                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/074,344
FILING DATE: 07-UNV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Effacient, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: VICAL.03
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/08403853
Patent No. 5844094
GENERAL INFORMATION:
APPLICANT: HUDSON, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
EBNGTH: 4965 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: circular
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KORRT, Alex A.
IRVING, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE:
ORIGINAL SOURCE:
STRAIN: HLA-B7 and Beta-2
PCT-US94-06069-1
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ADDRESSEE: Foley & Li
COMPUTER READABLE FORM:
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MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
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CLASSIFICATION:
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HYPOTHETICAL: NO
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STATE: D
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 GAGCTTGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGGGC 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.6%; Score 50; DB 2; Length 371;
100.0%; Pred. No. 4.4e-14;
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APPLICANT: Lodes, Michael J.
APPLICANT: Michael J.
APPLICANT: Michael J.
APPLICANT: Michael J.
APPLICANT: Michael J.
TYLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS FILE REPERENCE: 210121.466C2
CURRENT PELLING ANTE: 1999-09-16
NUMBER OF SEQ ID NOS: 334
SEQ ID NO 329
LENGTH: 438
LENGTH: 438
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Best Local Similarity 100.0%; Pred. No. 4.4.
Matches 50; Conservative 0; Mismatches
CLASSIFICATION: 435
PRICR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU93/00491
FILING DATE: 24-SEP-1993
PRICR APPLICATION NUMBER: WO PCT/AU93/00491
PRICING DATE: 25-SEP-1992
APPLICATION NUMBER: AU PL 4973
FILING DATE: 25-SEP-1992
ATTONNEY/AGRET TREPRANTION:
NAME: BENT, Stephen A.
RAGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16786/189/CHACTELCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRENCE: (202) 672-5399
                                                                                                                                                                                                                                                                                                         16786/189/CHAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 329, Application US/09397787; Patent No. 6468758; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: .c. TELEX: 904136
INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS: LENGTH: 371 base pairs TYPE: nucleic acid TYPE: nucleic acid STRANDEDNESS: single monogy: linear
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US-09-819-371-1
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Sequence 1806, Ap
Sequence 1806, Ap
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3713, Ap
Sequence 6712, Ap
Sequence 6712, Ap
Sequence 6712, Ap
                                                                                                      December 16, 2004, 14:31:28 ; Search time 672 Seconds (without alignments) 8946.715 Million cell updates/sec
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1: /cgn2_6/prodata/1/pubpna/PcT_RW PUB.seq:*
2: /cgn2_6/prodata/1/pubpna/PcT_RW PUB.seq:*
3: /cgn2_6/prodata/1/pubpna/PcT_RW PUB.seq:*
4: /cgn2_6/prodata/1/pubpna/USO7_NRW PUB.seq:*
5: /cgn2_6/prodata/1/pubpna/USO7_NRW PUB.seq:*
6: /cgn2_6/prodata/1/pubpna/USO7_NRW PUB.seq:*
7: /cgn2_6/prodata/1/pubpna/USO8_PUBCOMB.seq:*
8: /cgn2_6/prodata/1/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/prodata/1/pubpna/USO8_PUBCOMB.seq:*
10: /cgn2_6/prodata/1/pubpna/USO8_PUBCOMB.seq:*
11: /cgn2_6/prodata/1/pubpna/USO8_PUBCOMB.seq:*
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10: /cgn2_6/prodata/1/pubpna/USO8_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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5 US-10-172-118-1806

6 US-10-342-887-1806

1 US-09-819-371-2

1 US-09-819-371-3

1 US-09-819-371-3

1 US-09-819-371-3

1 US-09-880-107-3713

US-09-880-107-3713

5 US-10-257-071-81

6 US-09-764-891-6712

7 US-10-091-572-573

6 US-10-091-572-573

6 US-10-091-572-573
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                                                                                                                                                                                                                                                                                                                           4093002 seqs, 2760418825 residues
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                                                                       - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                OLIGO_NUC
Gapop_60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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APPLICANT: Egawa, Kohji
TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Can
TITLE OF INVENTION: Using Thereof
FILE REPRENCE: 30815
CURRENT APPLICATION NUMBER: US/09/819,371
CURRENT FILING DATE: 2002-03-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.0
  Sequence 4454, Ap Sequence 1888, Ap Sequence 13425, A Sequence 13425, A Sequence 13280, A Sequence 18890, A Sequence 539, App Sequence 1537, App Sequence 2148, App Sequence 289496, Sequence 289496, Sequence 289496, Sequence 289496, Sequence 289496,
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1089; Conservative 0; Mismatches 0; Indels 0;
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                                   ORGANISM: Homo sapiens
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; Sequence 1806, Application US/10172118; Publication No. US20030224374A1; GENERAL INFORMATION:

RESULT 2 US-10-172-118-1806 APPLICANT: Dai, Hongyue APPLICANT: He, Yudong APPLICANT: Linsley, Peter

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APPLICANT: Roberts, Chris
APPLICANT: Van 't Veer, Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Van de Vijver, Marc
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Ree
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 301-175-99
CURRENT FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1806
FERMAND: APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
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100.0%; Score 1089; Sest Local Similarity 100.0%; Pred. No. 0; Matches 1089; Conservative 0; Mismatches
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PUBLICATION INFORMATION:
DATABASE ACCESSION UNMSER: NM 018950
DATABASE ENTRY DATE: 2001-06-18
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APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: He, Yudong
APPLICANT: Mac, Mac
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APPLICANT: Mac, Mac
APPLICANT: Mac, Mac
APPLICANT: Non 't Veer, Laura Johanna
APPLICANT: Van de Vijevr, Marc J.
APPLICANT: Sandards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 3011-188 999
CURRENT APPLICATION NUMBER: 60/298,918
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 10/172,118
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NOS: 2699
LENGTH: 1188
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CORGANISM: Homo sapiens
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies, FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 589
LENGTH: 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 72.2%; Score 786; DB 9; Length 816; Best Local Similarity 100.0%; Pred. No. 0; Matches 786; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-301-589
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PARLICANT: Egawa, Kohji
TITLE OF INVENTION: Cancer Cell-Specific HLA-F Antigen and a Diagnostic Method of Canc
TITLE OF INVENTION: Using Thereof
FILE REPRENCE: 30015
CURRENT APPLICATION NUMBER: 2002-03-15
CURRENT FILING DATE: 2002-03-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.0
SEQ ID NO 2
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                                                                                             ; Sequence 2, Application US/09819371; Publication No. US20040053344A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
US-09-819-371-2
800 ACCTTC 805
                                                                                US-09-819-371-2
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384 ACGCCTCCTCCGCGGGTATCACCAGCACGCGTACGACGGCAAGGATTACATCTCCCTGAA 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 GCGGGAGCCGTGGGTGGAGCAAGAGGGCCCGCAGTATTGGGAGTGGACCACAGGGTACGC 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264 CAAGGCCAACGCACAGACTGACCGAGTGGCCCTGAAGGAACCTTGCTCCGCCGCTACAACCA 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            324 GAGCGAGGCTGGGTCTCACCCTCCAGGGAATGAATGGCTGCGACATGGGCCCGACGG 383
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Batent No. US20020142981A1

Fatent No. US20020142981A1

Fatent No. US20020142981A1

FAPELCANT: HORANTION:

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

ITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;

FILE REPERENCE: 44921-5028-WO

CURRENT APPLICATION NUMBER: US/09/880,107

CURRENT PILING DATE: 2000-06-14

FRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARR: PatentIn Ver. 2.1

SEQ ID NO 3713
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; Sequence 37854, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
APPLICANT: Hyeeq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: RROW VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/225,076
; PRIOR FILING DATE: 1999-010
; NUMBER OF SEQ ID NOS: 38054
; GOOT IN NO. 27064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (1)...(487)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-37854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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US-09-880-107-3713
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                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09819371

Publication No. US20040053344A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Cancer Cell-Specific HiA-F Antigen and a Diagnostic Method of Can
TITLE OF INVENTION: Using Thereof
TITLE REPERENCE: 30815
CURRENT APPLICATION NUMBER: US/09/819,371

NUMBER OF SEQ ID NOS: 6
SOPTWARE: Patentin version 3.0
SEQ ID NO 3.6
SEQ ID NO 3.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 TIGGGAGTGGACCACSGGGTACGCCAAGGCCAACGCACAGACTGACCGAGTGGCCCTGAG 170
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                         754 GGAGAGGAACAGAGATACACATGCCATGTGCAGCACGAGGGGCTGCCCCAGCCCCTCATC 813
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                                                                                                 877 CTGAGATGG 885
                                                                                                                                                                        814 CTGAGATGG 822
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                          RESULT 6
US-09-819-371-3
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US-09-819-371-3
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RESULT 7 US-09-918-995-37854

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; Sequence 6712, Application US/09764891; Publication No. US20030077808A1; GENERAL INFORMATION:
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Best Local Similarity 100.0
Matches 277; Conservative
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US-09-764-891-6712
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                                                                                                                                                                                                                                                                                                                                                                                 608 CAGATCCTCCAAAGGCACACGTTGCCCACCCCATCTCTGACCATGAGGCCACCTGA 667
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                                                                                                            ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X17093
US-09-880-107-3713
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                                                                                                                                                                                                                            / Match 25.6%; Score 279; DB 9; Length 4316; Local Similarity 100.0%; Pred. No. 7.8e-135; Nes 279; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 81, Application US/10257021
; Publication No. US20030211498A1
; GENERAL INFORMATION:
    APPLICANT: Morin, Patrice J.
    APPLICANT: Morin, Patrice J.
    APPLICANT: Hough, Patrice J.
    APPLICANT: Hough, Collean D.
    TITLE OF INVENTION: TUMOR MARKERS IN CVARIAN CANCER FILER OF INVENTION: TUMOR MARKERS IN CVARIAN CANCER CURRENT APPLICATION WIMBER: US/10/257,021
    CURRENT APPLICATION NUMBER: US/10/257,021
    CURRENT FILING DATE: 2002-10-03
    PRIOR APPLICATION NUMBER: 60/194,336
    PRIOR PALICATION NUMBER: 60/194,336
    PRIOR PRILICATION NUMBER: 60/194,336
    PRINCATION NUMBER: 60/194,030
    PRINCATION NUMBER: 60/194,030

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TYPE: DNA
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-257-021-81
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                                                                                FEATURE:
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2593 AGAAGTGGGCCCCTGTGGTGGTGCCTTCTGGAGAACAGAGAACAGAGAACACATGCCATGTGC 2652
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPRENCE: PALISC1
CURRENT APPLICATION NUMBER: US/10/091,572
CURRENT FILING DATE: 2002-03-07
PRIOR PRILOR TILING DATE: 2001-01-17
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-11
PRIOR FILING DATE: 2000-06-11
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCOOR
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6712
                                                                                                                                                                                                                                                                                                                             2653 AGCACGAGGGCTGCCCCAGCCCCTCATCCTGAGATGGG 2691
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Publication No. US20330194704A1
Sublication No. US20330194704A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GILLE REFERENCE: AEONICA-X-2
TITLE OF INVENTION: HUMAN GENOME-DAVISIS TWO
FILE REFERENCE: AEONICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
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OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12
OTHER INFORMATION: NT HIT: AF055066.1, EVALUE 0.000+00
OTHER INFORMATION: SWISSEROT HIT: P30511, EVALUE 6.000-53
OTHER INFORMATION: EST_HUMAN HIT: AV752612.1, EVALUE 0.000+00
US-10-029-38619154
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OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 12

OTHER INFORMATION: EST HUMAN HIT: AV752612.1, EVALUE 0.00e+00

OTHER INFORMATION: WHIT: X17093.1, EVALUE 0.00e+00

OTHER INFORMATION: SWISSPROT HIT: P30511, EVALUE 2.00e-52
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NUMBER OF SEQ ID NOS: 34286
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SOFTWARE: Annomax
Sequence Listing Engine vers. 1.1
LENGTH: 289
TYPE: DNA
ORGANISM: Homo sapiens
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LENGTH: 552
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99.6%; Pred. No. 4.3e-108;
tive 0; Mismatches 1;
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Best Local Similarity 99.69
Matches 278; Conservative
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US-10-029-386-18154
US-10-029-386-18154
Sequence 18154, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR OF TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: AECHICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
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25.4%; Score 277; DB 14; Length 3098;
Best Local Similarity 100.0%; Pred. No. 9e-134;
Matches 277; Conservative 0; Mismatches 0; Indels 0
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          PRIOR FILING DATE: 2000-11-17
PRIOR PLING DATE: 2000-05-14
PRIOR PLING DATE: 2000-05-14
PRIOR PLING DATE: 2000-05-14
PRIOR FILING DATE: 2000-09-08
PRIOR PLING DATE: 2000-09-08
PRIOR PLING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,244
PRIOR APPLICATION NUMBER: 60/231,64
PRIOR APPLICATION NUMBER: 60/233,064
PRIOR PLING DATE: 2000-09-14
PRIOR PLING DATE: 2000-10-20
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Sequence 33425, Application U8/10242535A

Publication No. U520040013663A1

GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: ChondroGene Inc.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002.
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
FRICH APPLICATION NUMBER: US 60/305,783
FRICH APPLICATION NUMBER: US 60/305,340
FRICH APPLICATION NUMBER: US 60/205,340
FRICH APPLICATION NUMBER: US 60/205,340
FRICH APPLICATION NUMBER: US 60/205,340
FRICH APPLICATION NUMBER: US 60/275,017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.8%; Score 85; DB 16; Length 561; Best Local Similarity 99.3%; Pred. No. 1.2e-33;
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NAME/KEY: misc_feature
LOCATION: (530).
OTHER INFORMATION: n equals a,t,g, or c
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; LOCATION: (541)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-264-049-1888
                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (491)..(491)
OTHER INFORMATION: n equals a,t,g, or
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NAMEKEY:
LOCATION: (525)..(525)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                                                                                                                                                         LOCATION: (523). (523)
OTHER INFORMATION: n equals a,t,g, or
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                                    NAME/KEY: misc feature
LOCATION: (445)..(445)
OTHER INFORMATION: n equals a,t,g,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 135; Conservative
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LOCATION: (523)..(523)
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; ORGANISM: Human
US-10-242-535A-33425
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LENGTH: 217
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                                    246 CAGATCCTCCAAAGGCACACGTTGCCCACCACCCATCTCTGACCATGAGGCCACCCTGA 305
                                                                                                                                                                        306 GGTGCTGGGCCTTCTACCCTGGGAAATCACGCTGACCTGGGGATGGGG 365
                                                                                                                                                                                                                                                                                                                      608 cagarcercaaaageaacacercaecaceaecaceaecarcercaeaecargaageceaecersa 667
                                                                                                                                       GGTGCTGGGCCTTGCGGCTTCTACCCTGCGGAGATCACGCTGACCTGGCAGCGGGATGGGGG 727
                                                                                                                                                                                                                                                                   728 AGGAACAGACCCAGGACACAGAGCTTGTGGAGACCAGGCCTGCAGGGGATGGAACCTTCC 787
                                                                                                                                                                                                                                                                                                                                                                                                       788 AGAAGTGGGCCGCTGTGGTGGTGCCTTCTGGAGGAACAGAGATACACATGCCATGTGC 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1884, Application US/10264049
; Publication No. US20040005579A1
; Publication No. US20040005579A1
; Publication No. US20040005579A1
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; CURRENT APPLICATION NUMBER: US/10/264.049
; CURRENT APPLICATION NUMBER: US (0/204, 467)
; PRIOR FILING DATE: 2001-06-07
; PRIOR FILING DATE: 2000-06-07
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: Patentin Ver. 3.1
; SEQ ID NO 1888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   486 AGCACGAGGGCTGCCCCAGCCCCTCATCCTGAGATGGG 524
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OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
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LOCATION: (231)...(231)
OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (2587..(258)
OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (374) )
OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (409)..(409)
OTHER INFORMATION: n equals a,t,g, or c
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OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (369)..(369)
OTHER INFORMATION: n equals a,t,g, or c
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LOCATION: (321). (321)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (137)..(137)
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Oy 957 CACTGGAGCTGTGGTCGCTGTGATGTGGAGGAAGAGGTCAGATAGAAACAGAGG 1016

Db 18 CACTGGAGCTGTGGTCGCTGTGATGTGGAGGAAGAGGTCAGATAGAAACAGAGG 77

Oy 1017 GAGCTACTCCAGGCTGCAGT 1037

Db 78 GAGCTACTCTCAGGCTGCAGT 98

Search completed: December 16, 2004, 17:19:21

Job time: 675 secs
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CD514705 AGENCOURT
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BQ711764 AGENCOURT
BG743996 602722769
CB529818 UI-H-FT2-
CB528498 UI-H-FT2-
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602627060
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                                                       December 16, 2004, 12:47:28 ; Search time 4075 Seconds (without alignments) 9738.127 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                             32822875 segs, 18219865908 residues
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                                     OM nucleic - nucleic search, using sw model
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BD688194
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CB528498
                                                                                                                                 OLIGO_NUC.
Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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6: 9b_est4: *: *
7: 9b_est5: *: *
9: 9b_gss1: *: *
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CD368629 CD368629 UI-H-FTI-BM72642 BM762642 BM46242 VEST0043 BM42679 CD367343 UI-H-FTI-10 CD367343 UI-H-FTI-10 BM456332 BM6831090 602766640 BM456334 AGBNCOURT 602741158 AM610235 AM610235 RC2-ST030 CB529146 BC705903 CD529146 BQ705603 CD529146 BC705903 CB529146 BC705903 CD714710 CA308000 BG75793 GO114974 CB52916 CD742770 CD742770 CB52916 BG75793 GO114974 CB52916 BM75793 GO114974 CB52916 CD742770 CD74277 CB52916 CD74277 CD74277 CB52916 CD74277 CD74277 CB52916 CD74277 CD74277 CB52916 CD74277 CD74277 CB52916 CD52916 CD74270 CB52916 CD74277 CD74277 CB52916	ALIGNWENTS	DESI470S AGENCOURT 1439444 NIH MOC_181 Homo sapiens CDNA clone UNAGE: 34040875 5', mRNA sequence. CD514705 EST 06-JUN-2003
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	7	CD514705 AGENCOURT 1439444 NIH MGC 18. IMAGE:30408575 5', mRNA sequences and sequences
8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		1 G1:314444 NIH 08575 5', mRN 1 G1:3144442 ens (human) ens 'Metazoa; Ch Eutheria' Pr Eutheria' Pr Intp://mgc.nci intp://m
R 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		CD514705 AGENCOURT 14394444 1 1MAGE:30408575 5', 1 CD514705. GI:3144 EST. Homo sapiens (human Homo sapiens Bukaryota; Metazoa; Mamalia; Butheria; 1 (Bases 1 to 829) 1 (Bases 2 to 829) 1 (Bases 3 to 829) 1 (Bases 3 to 829) 1 (Bases 4 to 820)
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/lab_host="DHIOB (phage-resistant)"
/clone lib="NHH MGC-113"
/clone lib="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5: dapptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis Kit (Stratagene) and
Superseript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 GGAGCAAGGGGGCCGCAGTATTGGGAGTGGACCACAGGTACGCCAAGGCAACGCACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          459 CTGGACCGCGGCGGACACCGTGGCTCAGATCACCCAGCGCTTCTATGAGGCAGAGGAATA 518
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                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDMA Library Preparation: Rubin Laboratory
CDMA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov n column: 06
High quality sequence stops: 628.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 CONGECCONGACCGANACTIGGGCGGGCTCCCACTCCTUGAGGTATTTCAGCACCGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 CCTGGCCCTGACCGATACTTGGGCGGGCTCCCACTCCTTGAGGTATTTCAGCACCGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98 GTCGCGGCCCGGCCGCGGGGAGCCCCGCTACATCGCCGTGGAGTACGTAGACGACGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 ATTCCTGCGGTTCGACAGCGACGCCGCGATTCCGAGGATGGAGCCGCGGGAGCCGTGGGT
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                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
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Best Local Similarity 100.0
Matches 757; Conservative
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1 (bases 1 to 926)

NIH-MGC http://mgc.nci.nih.gov/,
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                       ATGGCGCCCCGAAGCCTCCTCCTGCTCCTCAGGGGCCCCTGGCCCTGACCGATACTTGG
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                      Best Local Similarity 100.0%; Pred. No. 0; Matches 763; Conservative 0; Mismatches
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886 bp mRNA linear EST 15-JUL-2002
AGENCOURT 9064678 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6206180
BQ688194
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Contact: Robert Strausberg, Ph.D.
Email: cgapbe-remail.nih.gov
Tissue Procurement: ATCC
CORMALIbrary Preparation: Rubin Laboratory
CDRA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.G.E. Consortium/LLNL at:
http://image.llnl.gov d column: 21
High quality sequence stop: 677.
                                              163 CGCTCCTGGACCGCGGCGGACACCGTGGCTCAGATCACCCAGCGCTTCTATGAGGCAAAG 222
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutharia; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 886)
NIH-WGC http://mgc.nci.nin.gov/.
National Institutes of Health, Mammalian Gene Collection (WGC)
                                                                                                                                  514 GAATATGCAGAGGAGTTCAGGACCTACCTGGAGGCGAGTGCCTGGAGTTGCTCCGCAGA
                                                                                                                                                                      523 TCTGGAGAGCAACAGAGATACACATGCCATGTGCAGCACGAGGGGCTGCCCAGCCCCTC
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Bldg. 31 Rm10A07 Betheada, MD 20892
CDNA Library Preparation: Invitrogen Corporation
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencial by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM473 row: 1 column: 01
High quality sequence start: 8
High quality sequence stor: 707.
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          639 CCCCATCTCTGACCATGAGGCCACCCTGAGGTGCTGGGCCCTGGGCTTCTACCCTGCGGA 698
                                              638 CCCCATCTCTGACCAIGAGGCCACCCTGAGGIGCTGGGCCCTGGGCTTCTACCCTGGGGA 697
                                                                                                                                            GATCACGCTGACCTGGCAGCGGGATGGGGAAGGAACAGACCCAGGACACAGAGCTTGTGGA 758
                                                                                                                                                                                                   698 GATCACGCTGACCTGGCAGCGGGATGGGGAACAGACCCAGGACACACAGACCTTGTGGA 757
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 897)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD512828
AGENCOURT_14373093 NIH_MGC_179 Homo sapiens CDNA clone
IMAGE:30394728 5', mRNĀ seguence.
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                                                                                                                                                                                                                                                                       759 GACCAGGCCTGCAGGGGATGGAACCTTCCAGAAGTGG 795
                                                                                                                                                                                                                                                                                                                   758 GACCAGGCCTGCAGGGATGGAACCTTCCAGAAGTGG 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
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/clone="IMAGE:6206180"
/tissue_type="ductal carcinoma, cell line"
/lab host="H108 (phage-resistant)"
/clone_lib="NHMGC_110"
/clone_lib="NHMGC_110"
/clone_lib="NHMGC_110"
/note="Organ: pancreas; Vector: pOTB7; Site_l: Khôl;
Site_2: EcoRi, cDNA made by oligo-dr priming.
Directionally cloned into EcoR//Khol sites using the following s' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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DEFINITION ACCESSION

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//organism="Homo sapiens"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1130)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM2011 row: g column: 20
High quality sequence stop: 644.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: ogapbs-r@mail.nih.gov
Tissue Procurement: Dr. Daniel McVicar, DBS/NCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.1%; Score 654; DB 100.0%; Pred. No. 0; tive 0; Mismatches
GI:19367451
                                                                                     Homo sapiens (human)
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Best Local Similarity
                                                                                                                                    Homo sapiens
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the disconting of the control of the	121 CCCGGCTACATCGCCGTGGAGTACGTAGGGGACGACGCAATTCCTGCGGGTTCGACGCGAC 180	147 CCCCGCTACATCGCCGTGGAGTACGTAGACGACACGCAATTCCTGCGGTTCGACAGCGAC 206	181 GCCGCGATTCCGAGGATGGAGCCGCGGGGGGCCGTGGGTGG	-0	241 TGGGAGTGGACCACAGGGTACGCCAAGGCCAACGCACGACTGACCGAGTGGCCCTGAGG 300	267 iddakordakakakakakakakakakakakakakakakakakakak	301 AACCTGCTCCGCCGCTACAACCAGAGCGAGGCTGGGTCTCACACCCTCCAGGGAATGAAT	GACTTACKS CATTAGAGACT CASA CACTACTTCCCCGGGT AT CACTACTACTACTACTACTACTACTACTACTACTACTACT	GGCTGCGACATGGGGCCCGACGGCCTCCGCGGGTATCACCAGCACGGGTACGAC	421 GGCAAGGATTACATCTCCCTGAACGAGGACCTGCGCTCCTGGACCGCGGGGGGACACCGTG 480	447 dáchadánttachterecetéhadéahácetácaétéchéahácadádáhátacetá 506	481 GCTCAGATCACCCAGCGCTTCTATGAGGCAGAGGAATATGCAGAGAGTTCAGGACCTAC 540	541 CTGGAGGGCGAGTGCCTGGAGTTGCTCCGCAGATACTTGGAGAATGGGAAGGAGACGCTA 600	#1.79.74.79.49.79.79.79.79.79.79.79.79.79.79.79.79.79	601 CAGCOGGLAGATCGTCCAAAGGCACATGCTGCTACCCCATCTCTGGCGCATGGGGCC 660	ACCTGAGGTGCTGGGCCCTGGGCTTCTACCCTGCGGAGATCACGCTGACCTGCCAGCGG	⋖	721 GATGGGGAGGAACAGACCCAGGACACAGAGCTTG 754 		LOCUS BQ710481 925524 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:6279516 C, mbNA ferroCNFT 835524 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279516 C, mbNA ferromence				ENCE 1 (Bases I Co 928) HORNS NIH-MGC http://mgc.nci.nih.gov/. LE National Institutes of Health, Mammalian Gene Collection (MGC)	Ar.	CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequenoing by: Agencourt Bioscience Corporation	Clone distribution: McC clone distribution information can be found through the I.M.A.G.E. Consortium/LIND at:	nttp://lmage.lln.gov Plate: LLCM2469 row: d column: 13 High quality sequence stop: 647.
439 GCTCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ò	q	ò	q	δō	q	රු සි	Ş	g 90	ò	qq	ζζ Q	\$ 5	3	හි සි	δ i	Q C	රු පි	RESUL BO710	LOCUS	ACCES VERSI	SOURC		KEFEKEN AUTHO TITLE	JOURN COMMENT			
1 1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		GCTCAGAICACCCAGCGCTTCTAIGAGGCAGAGGAATATGCAGAGGAGTTCAGGACCTAC 54	dereagareaceagegerrerargadgeagagarargeagaggarreagagerae	CTGGAGGGCGAGTGCCTGGAGTTGCTCCGCAGATACTTGGAGAATGGGAAGGACGCTA	CTGGAGGGCGAGTGCCTGGAGTTGCTCCGCAGATACTTGGAGAATGGGAAGGAGGACGCTA	CAGGGGCAGATCCTCCAAAGGCACACGTTGCCCACCACCCCATCTCTGACCAT	609 CAGCGCGCAGATCCTCCAAAGGCACATTGCCCACCACCATCTCTGAGCAT		BM561951 BM561951 BM		BST. Homo sapiens (human)	SM Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	E 1 (Dases 1 to 949) S NHH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)	Contact: Robert Strausberg, Ph.D.	Emall: Gapbs-r@mail.nih.gov Tissue Procurement: Dr. Daniel McVicar, DBS/NCI CDNA Library Preparation: Rubin Laboratory	CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be	<pre>round through the 1.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov</pre>	Plate: LLCW2013 row: o column: 02 High quality sequence stop: 682. Location/Qualifiers	/ r. gran = "Homo sapiens" /mol_type="mRNA" /db xref="taxon:9606"	/clone="IMAGE:5484505" /tissue_type="mateural killer cells, cell line" /lab host="DH108 (phage-resistant)"	/clone_lib="NIH MGC_16" /clone_logan: blood; Vector: poTBC_16" /cote-"Cons." All of Vector: poTBC_16"	ECOLI, CDNA Made by Oligo-di priming. Directionally cloned into Ecolf/Khol sites using the following 5, adaptor: GGCACAG(G). Library constructed by Ling Hong in the	laboratory of Gerald M. Rubin (University of California, Berkeley) using SAP-cDNs kit (Stratagene) and Berkeley) and California (Titom (Titom California))	Superscript 11 K1 (Life reconologies). Note: Chis is a NH_MGC Library."	tch 59.9%; Score 652; DB 4; Length 949; sal Similarity 99.7%; Pred. No. 0; 752; Conservative 0; Mismatches 2; Indels 0; Gaps	TICCTGCTGCTCTCAGGGCCTGGCCCTGACCGATACTTGG	9 0	

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BG679105 T18 bp mRNA linear EST 01-MAY-2001 000827001 NCI_CGAP_SKN4 Homo sapiens cDNA clone IMAGE:4752038 5',
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                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 718)
                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-remail.nih.gov
Tissue Procurement: Janes Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10609 row: g column: 15
High quality sequence stop: 715.
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                                                                                                                                                                                                                                                                                                                             NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/mol type≈"mRNA"
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'db_xref="taxon:9606"
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                                                                                                                                                                                                                        Homo sapiens (human)
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ses 642; Conservative
                                                                                                                                 mRNA sequence.
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                                                                                                     /clone="Image:6279516"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lone="lib="NIH MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: spleen; Vector: priming. Directionally cloned
into EcoRI; Chan made by oligo-dT priming. Directionally cloned
into EcoRI/Xhol iste using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                             'organism="Homo sapiens"
                                                              Ltype="mRNA"
xref="taxon:9606"
ocation/Qualifiers
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    4 ATGGCGCCCCGAAGCCTCCTCCTGCTGCTCTCAGGGGCCCTGGCCCTGACCGATACTTGG 63
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.lln.gov
Plate: LLCM2567 row: p column: 23
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
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Matches 785; Conservative
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AUTHORS
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/dlone=InAdGE:628481"
/tissue type="ductal carcinoma, cell line"
/lab host="mild (phage-resistant)"
/clone lib="NHLMS (phage-resistant)"
/clone lib="NHLMSC 110"
/note="Organ: pancreas; Vector: pOTB7; Site_1: Xho1;
Site_2: ExoRI; cDNA made by oilgo-dr priming.
Directionally cloned into Ecomi/Abol sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Ling Hong in the laboratory using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BQ690438 15-JUL-2002 AGENCOURT 8343876 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:62484815, mRNA Sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 CCGCGATTCCGAGGATGGAGCCGCGGGAGCCGTGGGTGGAGCAAGAGGGGCCGCAGTAT 240
                    615 CAGCGCGCAGATCCTCCCNAAGGCACACTTGCCCACCACCACCATCTCTGACCATGAGGGC 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 cadscreceaerectreaddaararacageaeceerergregeegeegeegeegeegeege 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

I Chases, 1 to 892)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mailih.gov

Tissue Procurement: ATCC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCNASSB row: g column: 10
High quality sequence stop: 623.
High quality sequence stop: 623.
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                               675 Accercaderecredecere 695
                                                                                                                                                                 661 ACCCTGAGGTGCTGGGCCCTG 681
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BQ690438
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NHH MGC 18"
/note="Organ: lung: Vector: pOTB7; Site 1: XhoI; Site 2:
EcoR1; cDNA made by oligo-dT priming. Directionally cloned
into EcoR1/XhoI sites using the following 5, adaptor:
GCGCGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Burkeley) using ZAP-cDNA synthesis Kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  435 GGCAAGGATTACATCTCCCTGAACGAGCACCTGCGCTCCTGGACCGGGGGGGACACCGTG 494
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Tissue Procurement: DCTD/DTP/Gazdar

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)

DNA Sequencing by: Apencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM2604 row: e column: 14

High quality sequence stop: 638.
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/db_xref="taxon:9606"
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602246074F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4336866 5', mRNA sequence.
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1 (Dases 1 to 645)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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56.3%; Score 613; DB 1; Le
Best Local Similarity 100.0%; Pred. No. 5.6e-296;
Matches 613; Conservative 0; Mismatches 0;
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I (bases 1 to 79)

Song, H., Peng, Y., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Fu, G., Ren, S., Zhong, M., Lu, G., Ye, M., Tu, T., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Ye, M., Tu, C., Han, Z., Chen, J., Homo sapiens NPD library cDNA clones

I Homo sapiens NPD library cDNA clones

Contact: Qinghua Zhang
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197 Rui-Jin II Road, Shanghai 200025, P. R. China

Fax: 86-21-6443206

Email: mbshi@ms.stn.sh.cn
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                                                         241 GGGAGTGGACCACAGGGTACGCCAAGGCCAACGCACAGACTGACCGAGTGGCCTTGAGGA 300
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/dev stage="Adult"
/lab_hos="SODR"
/clone_lib="NDD"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                   GGGAGTGGACCACAGGGTACGCCAAGGCCAACGCACAGACTGACGAGTGGCCCTGAGGA 301
                                                                                                                                GCAAGGATTACATCTCCCTGAACGAGGACCTGCGCTCCTGGAACGGCGGCGGACACGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi- Tech Park, Pudong.
1. .790
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NPDASF03"
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Homo sapiens
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                                                                                                                                                                                                                                                    /tissue type="pinguage" line from tonsils (cell line)"
/lab host="DHIDB (phage-resistant)"
/lab host="DHIDB (phage-resistant)"
/clone_lib="NIH_MGC_del"
/note="Organ: B-cells vector: poTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the collowing 5' adaptor: GGCACGAG(G). Size-selected >500pp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis Xit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov d column: 19
Plate: LLGML210 row d column: 19
High quality sequence stop: 645.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.1%; Score 611; DB 2; Length 645; 100.0%; Pred. No. 5.7e-295; tive 0; Mismatches 0; Indels
                                                                                                                                                                          'organism="Homo sapiens"
                                                                                                                                                                                                                                        clone="IMAGE:4336866"
                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
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616 bp mRNA linear EST 05-JAN-2001
bx14a11.y1 Human Iris cDNA (Un-normalized, unamplified): BX Homo
saptens cDNA clone bx14a11 5', mRNA sequence.
BF725277
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tissue was pooled from 10 individuals ranging in age from
4-80 years and RNA was extracted. From this pooled sample
an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A
directionally cloned cDNA library in the pCMVSPORIG vector
was constructed at Life Technologies, essentially
following the protocols of the SuperScript Plasmid System
full details of which are contained in the manufacturer's
Instruction manual (http://www.lifetech.com/). First
strand synthesis was carried out using a Not I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [5.-pgACTAGTTCTAGATCGCGAGCGCCC(T)15-3']. Not I/blunt end inserts were cloned into the Not I/EcoR V sites in the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Iris"
/dev_arage="Adult"
/lab_host="EMDH108"
/clone_lib="Human Iris cDNA (Un-normalized, unamplified):
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1 (bases 1 to 636)
Wistow, G.J., Bernstein, S., Behal, A. and Smith, D.
NEIBANK: BST analysis and bioinformatics for ocular genomics Invest. Ophthalmol. Vis. Sci. 41 (2000) In press
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Section on Molecular Structure and Function
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56.0%; Score 610; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 1.8e-294;
Matches 610; Conservative 0; Mismacches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           National Eye Institute
6/31, NH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: graeme@helix.nih.gov
plate: 14 row: a column: 11
Seg primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="bx14a11"
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                                                                                                                                                                                                                    Homo sapiens (human)
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AUTHORS
TITLE
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COMMENT
RESULT 14
BF725277
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KEYWORDS
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/dev_stage="Adult"
/lab_hosts="BMDH10"
/clone_lib="Human Retinal pigment epithelium/choroid cDNA (Un-normalized, unamplified): cs"
                                                           420
                                                                                                                                                                                                                                                                                                                         540
TGGGAGTGGACCACAGGGTACGCCAAGGCCAACGCACAGACTGACCGAGTGGCCCTGAGG 300
                                                                                                       387 GGCTGCGACATGGGGCCCGACGGACGCCTCCTCCGCGGGTATCACCACGCGTACGAC
                                                                                                                                                                                                                                                  GGCAAGGATTACATCTCCCTGAACGAGGACCTGCGCTCCTGGACCGGCGGCGGACACCGTG 480
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 612)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wistow, G., Bernstein, S.L., Wyatt, M.K., Farris, R.N., Behal, A., Touchman, J.W., Bouffard, G., Smith, D. and Peterson, K. Expressed sequence tag analysis of human RPE/choroid for the NEIBank Project: Over 6000 non-redundant transcripts, novel genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cs16b02.yl Human Retinal pigment epithelium/choroid cDNA
(Un-rormalized, unamplified): cs Homo sapiens cDNA clone cs16b02
5', mRNA sequence.
CA391513
                                                                                                                                                                              GGCTGCGACATGGGGCCCGACGGACGCCTCCTCCGCGGGTATCACCAGCACGCGTACGAC
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Section on Molecular Structure and Function
National Eye Institute
6.331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
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Plate: 16 row b column: 02
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="cs16b02"
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/note="Organ: Eye; Vector: pCMVSPORT6; Two different donor eyes (75-60 years old) yielded approximately 600 mg of dissected RPE/choroid tissue. This in turn yielded 340 ug of total RNA and 7 ug of mRNA. A directionally clored cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies (Rockville, MD: now part of Invitrogen Corp), essentially following the protocols of the SuperScript Plasmid System (Invitrogen Corp. Rittp://www.invitrogen.com/>). The library code designation was cs. For this library, cDNA inserts were cloned into the NotI/Nul sites of the Vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
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